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Title:
Perfect score:
Sequence:
                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                  Database :
                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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pIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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913
1 RGDLMFLLDSSASVSHYEFS.....FVDVDDLHIIVQELRGSILD 180
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                                                                                                                                                                                                                                                                                                   283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	<u>ر</u>	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	(J	4	w	2	1	No.	Result
	Π.	_	152.5	153	158	5	159.5	62	53	168	175	175	179	184	191.5	194	198	198.5	207.5	214	16.	227.5	33.	39.	47.	54.	65.	65.	65.	Score	
				٠	٠	٠	17.5	•				•	٠	•	21.0	٠	•	•		•	•	24.9		•		•		29.1	29.1	Match	Query
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A33330	22200		G00039	156126	A45638	S44142	800551	I45914	RWHU1B	S42373	A88396	A48569	T23760	A35854	A40970	A45226	A55348	I51027	CGHU3A	T46488	A37797	**	A37979	\sim	A33809	A45974	A40020	4	2	ID	
inceditii aibiia-z c	מלכו מולים	cell surface glyco	von Willebrand fac	lymphocyte fuction	immunodominant mic	VLA-2 protein homo	leukocyte surface	integrin alpha 2 s		hetical	M01E10.2	antigen Em100 - Ei	ical prot	integrin alpha-1 c	undulin 1 - human	integrin alpha-1 c	integrin alpha-1 -	type XII collagen	alpha 3	hypothetical prote	lagen alpha	alpha 1	matrix	matrix	matri	lpha 1	collagen alpha 1(X	ä	collagen alpha 1(X	Description	

			42 98.5	٠											
10.5	10.5	10.6	10.8	10.9	10.9	11.3	11.4	12.0	12.2	12.4	14.6	14.6	15.3	15.3	15.8
1022	918	1025	371	1019	475	1028	643	567	13055	640	1170	1179	191	414	2813
Ν	N	N	N	۲	N	۲	N	N	N	N	N	N	N	N	س
S04111	S23377	S34839	S32604	A32856	T36921	CGHULA	T19549	T28797	T16580	T29784	S03308	A53213	I47230	PS0323	VWHU
collagen alpha 2(V	collagen alpha 2(V	collagen alpha 1(V	collagen alpha 2(V	collagen alpha 1(V	hypothetical prote	collagen alpha 1(V	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	cell surface glyco	integrin alpha-E c	VLA-2 protein - pi	von Willebrand fac	von Willebrand fac

ALIGNMENTS

278 SULT 2 8476 llagen alpha	Qy 63 GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSDPVGP 122	Query Match 29.1%; Score 265.5; DB 2; Length 1857; Best Local Similarity 34.5%; Pred. No. 2.2e-15; Matches 61; Conservative 33; Mismatches 82; Indels 1; Gaps 1; Qy 3 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 62 :: : : : : : : : : :	RESULT 1 Saliza collagen alpha 1(XIV) chain precursor, short form - chicken Collagen alpha 1(XIV) chain precursor, short form - chicken Collagen alpha 1(XIV) chain precursor, short form - chicken Collagen alpha 1(XIV) chain precursor, short form - chicken Collagen alpha 1(XIV) chain precursor, short form - chicken Collagen alpha 1(XIV) chain precursor, short form - chicken Collagen alpha 1(XIV) chain precursor, short form - chicken Collagen alpha 1(XIV) chain, short form - chicken Collagen XIV. Rate Complete primary structure of chicken collagen XIV. R. Waselchii, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. River J. Shochem. 212, 483-490, 1993 R. Waselchii, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. R. Waselchii, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. R. Waselchii, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. R. Waselchii, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. R. Rate J. Shochem. 212, 483-491, MUID:93185668; PMID:844186 A. Residues: nucleic acid sequence not shown; translation not shown A. Reference number: \$31211, MUID:93185668; PMID:844186 A. Residues: nucleic acid sequence not shown; translation not shown A. Reference number: \$31212, MUID:93185668; PMID:9444186 A. Residues: 1.1857 www.male.cha/www.male.cha/waselcha/ A. Residues: 1.1857 www.male.cha/waselcha

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F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1889/Product: collagen alpha 1(XIV) chain, long form #stat:
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3B>
F;623-707/Domain: fibronectin type III repeat homology <FN3B>
F;741-823/Domain: fibronectin type III repeat homology <FN3B>
F;32-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
                      A;Molecule type: mRNA
A;Residues: 1-3124 <YAM>
A;Cross-references: UNIPROT:Pl3944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810;
A;Coss-references: UNIPROT:Pl3944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810;
A;Cross-references: UNIPROT:Pl394; UNIP
                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The complete primary structure of type XII collagen shows a chimeric molecule nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site A;Reference number: A40020; MUID:92011862; PMID:1918137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: fibrochimerin C;Species: Gallus gallus (chicke
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A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: UNIPARC:UPI00001773F4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete primary structure of chicken collagen XIV A;Reference number: S31211; MUID:93185668; PMID:8444186 A;Accession: S31211
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A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793;
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Blochem. 212, 483-490, 1993
                                                                                                                                                                                                                                                                                                                                              A; Accession: A40020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Yamagata, M.; Yamada, K.M.;
J. Cell Biol. 115, 209-221, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen alpha 1(XII) chain precursor - chicken
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A;Accession: S78476
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;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
;Accession: S78476; S31211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811; Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Gallus gallus (chicken)
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factor type A repeat homology
    PMID:2584192
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F;2028-2110/Domain:
F;2119-2199/Domain:
F;2207-2294/Domain:
                                                                                                                                                                         F;1847-1928/Domain:
                                                                                                                                                                                                             F;1655-1738/Domain:
F;1756-1838/Domain:
                                                                                                                                                                                                                                                                                                      F;1566-1647/Domain:
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F;332-414/Domain: fibronectin type III repeat homology <FN3B>
F;437-601/Domain: von Willebrand factor type A repeat homology <
F;629-1178/Domain: IIIC #status predicted <IIIC>
F;630-711/Domain: fibronectin type III repeat homology <FN3C>
F;721-802/Domain: fibronectin type III repeat homology <FN3D>
F;721-802/Domain: fibronectin type III repeat homology <FN3E>
F;812-895/Domain: fibronectin type III repeat homology <FN3F>
F;915-986/Domain: fibronectin type III repeat homology <FN3F>
F;905-1076/Domain: fibronectin type III repeat homology <FN3H>
F;1096-1169/Domain: fibronectin type III repeat homology <FN3H>
F;1097-1361/Domain: von Willebrand factor type A repeat homology
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F;24-105/Domain: fibronectin type III repeat homology <FN3A>
F;137-301/Domain: von Willebrand factor type A repeat homology
F;137-425/Domain: IIIB #status predicted <IIIB>
F;332-425/Domain: IIIB #status predicted <IIIB>
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R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA
A;Reference number: A28037; MUID:87317590; PMID:3476925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1 C;Keywords: alternative splicing; cell binding; coiled coil; connective t F;1-23/Domain: signal sequence #status predicted cSIG>
F;24-3124/Product: collagen alpha 1(XII) chain #status predicted cMAT>
F;24-3124/Product: collagen alpha 1(XII) chain #status predicted cMAT>
F;24-1189-3124/Product: collagen alpha 1(XII) chain short splice form #st
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A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
A;Cross-references: UNIPARC:UPI00001712F4; EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A:Note: this sequence has been revised in reference A34485
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A;Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
A;Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45
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A;Title: A major oligomeric fibroblast proteoglycan identified
A;Reference number: S23814; MUID:92362621; PMID:1323460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU:
A;Cross_references: UNIPARC:UPI0000173C46; EMBL:X67327
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A;Title: The two splice variants of collagen XII share a common
A;Reference number: S28811; MUID:93042014; PMID:1420368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation
A;Reference number: S22254; MUID:88087065; PMID:3121603
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A; Residues: 2772-2792; 2846-2873 <GOR2>
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A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: UNIPARC:UP10000171233; EMBL:J05137; NID:g211284; PIDN:AAA48635.1;
if fibronectin type III repeat ho
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thomology <FN3L>
thomology <FN3M>
thomology <FN3N>
thomology <FN3O>
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Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
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F;2438-2440/Region: cell adhesion #status predicted
F;2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status
F;2751-2902/Domain: collagenous COL2 #status predicted <COL2>
F;2899-2901/Region: cell attachment (R-G-D) motif
F;2909-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F;2946-3048/Domain: non-collagenous NC1 #status predicted <NC1>
F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F;3780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (R)
                                                                                                   R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class A;Reference number: $17035; MUID:92037585; PMID:1935930
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C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, J. Biol. Chem. 268, 12177-12184, 1993
                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 286-494,'Q', 496-834,'A', 836-1119,'KL', 1122-1402,1409-1439
A; Cross-references: UNIDARC: UP10000173C48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, March 1992 A;Reference number: $30085 A;Accession: $30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000173C47
A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide transla
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A; Residues: 1472-1660 < APT>
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                          A; Residues: 1472-1659 < GOR1 >
                                                   A; Molecule type: mRNA
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Matches 62
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Cross-references: UNIPARC:UPI0000173C49
                                                                                Accession:
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A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rosidues: 1551-1570;1593-1599;1639-1667 <GOR2>
A;Cross-references: UNIPARC:UPI0000173C49
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime F;40-204/Domain: von Willebrand factor type A repeat homology <FW3A>
F;326-317/Domain: fibronectin type III repeat homology <FW3B>
F;326-317/Domain: fibronectin type III repeat homology <FW3B>
F;418-498/Domain: fibronectin type III repeat homology <FW3B>
F;507-591/Domain: fibronectin type III repeat homology <FW3B>
F;716-798/Domain: fibronectin type III repeat homology <FW3B>
F;716-798/Domain: fibronectin type III repeat homology <FW3B>
F;327-1099/Domain: fibronectin type III repeat homology <FW3B>
F;327-1089/Domain: fibronectin type III repeat homology <FW3B>
F;3111-1352/Domain: von Willebrand factor type A repeat homology <WA2>
F;1111-1352/Domain: non-collagenous NC2 #status predicted <NC4>
F;1511-1553/Domain: triple helical domain COIl #status predicted <COLl>
                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P05099; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; GB:R,Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.

Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987

A;Title: Structural features of cartilage matrix protein deduced from cDNA.

A;Reference number: A26364; MUID:87092429; PMID:3025875

A;Accession: A26364

A;Molecule type: mRNA

A;Residues: 78-493 <ARG>
A;Residues: 78-493 <ARG>
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A

F;37-204/Domain: von Willebrand factor type A repeat homology <VWAl>
F;225-260/Domain: EGF homology <EGF>
F;225-260/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cartilage matrix protein precursor - chicken
(;Species: Gallus gallus (chicken)
(;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
(;Accession: A33809; R26364
R;Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimbern
J. Biol. Chem. 264, 8126-8134, 1989
A;Title: Structure of the gene for cartilage matrix protein, a modular proteins, Von Willebrand factor, complement factors B and C2, and epidermal gr.
A;Reference number: A33809; MUID:89255246; PMID:2542265
A;Accession: A33809; MUID:89255246; PMID:2542265
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F;270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
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A; Residues: 1-493 < KIS>
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Best Local S
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DLVFLIDGSKSVRPENFELVKKFINQIVESLEVSEKQAQVGLVQYSSSVRQEFPLGQFKN
                                                         DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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                                                                                                                                                27.1%; Score 247.5; 38.0%; Pred. No. 2e-
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                                                                                                             Pred. No. ze-
2; Mismatches
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Pred. No. 2e-
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A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1 C;Complex: homotrimer C;Superfamily: cartilage matrix protein; EGF homology; vo
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C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                        A; Cross-references: GDB:127280; OMIM:115437
                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 157-290, 'L',292-496 <JE2>
A;Cross-references: UNIPARC:UPI000016A6E8;
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A; Residues: 1-500 < ASZ>
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A;Residues: 1-496 <JEN>
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                                                                                                                                                                                                                                                   ;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem. 265, 19624-19631, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 DIMFLIDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRDVSERARASGIELFAIGLGRVDKATLRQIASEPQDEHVDYVE 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing and
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34.8%; Pred. No. 1e-1
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g and expression analysis of mouse cartilage matrix protein MUID:96270751; PMID:8665920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location of the human gene
                                                                                                                                                                                                                                                                                    GB:M55683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 le-13;
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                                                                                                                                                                                                                                                                                        GB:J05666;
        von
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        Willebrand
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        factor
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C; Keywords: (F; 1-22/Domai)
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F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;76,344/Binding site: carobhydrate (Asn) (covalent) #status predicte
F;76,344/Binding site: carobhydrate (Asn) (site carobhydrate)
F;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;23-496/Product: cartilage matrix protein #status predicted <MAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWA
                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                        ocal
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                                                                                                                                     63 GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein; homotrimer
                                                                                                                                                                                                                               3 DIMFILDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 62
                                                                                                                                                                                                                                                                             62; Conserv
AAKKAKDLGFKMFAVGVGNAVEDELREIASEPVAEHYFYTADFKTINQIGKKLQKKI
                                           PMOELKDLGVTVFIVSTGRGNFLELSAAASAP-AEKHLHFVDVDDLHIIVQELRGSI 178
                                                                                              KKDIKAAVRNMSYMEKGTMTGAALKYLIDNSFTVSSGARPGAQKVGIVFTDGRSQDYIND 394
                                                                                                                                                                                        DLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQVGLVQYSSSVRQEFPLGRFHT 334
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                        25.6%;
35.0%;
                                                                                                                                                                                                                                                                                  27; Mismatches
                                                                                                                                                                                                                                                                                                     Score 233.5; DB 2
Pred. No. 3.5e-13;
                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                  87;
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  451
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Collagen alpha 1(VII) chain precursor - human
N;Alternate names: procollagen alpha 1(VII) chain
C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 ##equence revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54849; PH0844; \overline{S}16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the A;Reference number: A54849; MUID:94327588; PMID:8051117
A;Accession: A54849 A;Cross-references: UNIPROT:Q02388; UNIPARC:UPI000017A138; A; Molecule type: mRNA A; Residues: 1-2944 < CHR > A; Status: not compared with conceptual translation œ GB:L02870; NID:G987124; PIDN the alpha1(VII)

R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A;Title: Molecular cloning and characterization of type A;Reference number: PH0844; MUID:92231902; PMID:1567409 A; Accession: PH0844 VII collagen

A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 'EFR', 340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C'
A;Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:l
A;Experimental source: keratinocyte
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mal
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316 :B/

Mati

A;Cross-references: UNIPARC:UPI000016A722; GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96 A; Molecule type: mRNA A; Residues: 815-892, 'E', 894-1439 < PAR>

A;Experimental source: keratinocyte R;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E. J. Invest. Dermatol. 99, 691-696, 1992 A;Title: Noncollagenous (NCl) domain of collagen VII resembles multidomain A;Status: translated from GB/EMBL/DDBJ A;Reference number: I56328; MUID:93107742; A;Accession: I56328 Cook, M.E.; Wright, adhesion prot J.;

J. Biol. A;Title: A; Molecule type: mRNA A; Residues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 < RES> A; Cross-references: UNIPARC: UPI000016B3AC; GB: S51236; NID R; Seltzer, J.L.; Elsen, A.Z.; Bauer, E.A.; Morris, N.P.; (R; Seltzer, J.L.; Elsen, A.Z.; Bauer, E.A.; Morris, N.P.; (J. Bibl. Chem. 264, 3822-3826, 1989 Chem. 264, 3 Cleavage of collagen γģ interstitial collagenase GB:S51236; NID:g262308; Morris, N.P.; Glanville, and PIDN:AAB24637.1; , R.W.; Burgeson, type IV collagenas PID:

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Fig. 201/Domain: communication incumentation for the predicted (NCL)

Fig. 201/Domain: fibronectin type III repeat homology <PN1>
Fig. 201/Domain: fibronectin type III repeat homology <FN1>
Fig. 27-413/Domain: fibronectin type III repeat homology <FN2>
Fig. 414-502/Domain: fibronectin type III repeat homology <FN3>
Fig. 68-93/Domain: fibronectin type III repeat homology <FN3>
Fig. 68-93/Domain: fibronectin type III repeat homology <FN4>
Fig. 68-93/Domain: fibronectin type III repeat homology <FN6>
Fig. 68-771/Domain: fibronectin type III repeat homology <FN7>
Fig. 68-771/Domain: fibronectin type III repeat homology <FN8>
Fig. 68-952/Domain: fibronectin type III repeat homology <FN9>
Fig. 68-952/Domain: fibronectin type III repeat homology <FN9>
Fig. 68-952/Domain: fibronectin type III repeat homology <FN9>
Fig. 68-952/Domain: fibronectin
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A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A:Note: two reported peptides cannot be reliably located
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F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F;17-1253/Domain: amino-terminal nonhelical #status predicted <NCI>
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A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
A;Note: there are 118 introns
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A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser A;Reference number: A55255; MUID:94224777; PMID:8170945
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A;Title: The carboxyl-terminal half of type VII collagen, A;Reference number: I48103; MUID:93271985; PMID:8499916
A;Accession: I84686
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A; Residues: 2395-2871, 'S', 2873-2944 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Greenspan, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complex: type VII collagen is probably a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
    121
                                                                                                  98 GSGGDVIRAIRELSYKGGNTRTGAAILHVADHVFLPQL-ARPGVPKVCILITDGKSQDLV
                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                        38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,2804/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                 3 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGA--LRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                              DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
                                                                                                                                                                                           SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 227.5; DB 2;
Pred. No. 9.7e-12;
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157 DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVN
 199
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F;239-404/Domain: von Willebrand factor type A repeat homology < VW02>
F;442-607/Domain: von Willebrand factor type A repeat homology < VW03>
F;442-607/Domain: von Willebrand factor type A repeat homology < VW04>
F;840-1004/Domain: von Willebrand factor type A repeat homology < VW04>
F;1033-1197/Domain: von Willebrand factor type A repeat homology < VW05>
F;1039-1400/Domain: von Willebrand factor type A repeat homology < VW07>
F;1439-1604/Domain: von Willebrand factor type A repeat homology < VW08>
F;1639-1804/Domain: von Willebrand factor type A repeat homology < VW08>
F;1639-1804/Domain: von Willebrand factor type A repeat homology < VW09>
F;1838-2010/Domain: von Willebrand factor type A repeat homology < VW10>
F;2043-2378/Domain: von Willebrand factor type A repeat homology < VW10>
F;2045-2047/Region: cell attachment (R-G-D) motif
F;2153-2155/Region: cell attachment (R-G-D) motif
F;2159-2161/Region: cell attachment (R-G-D) motif
F;2163-2806/Domain: non-collagenous #status predicted <CNC>
F;2633-2806/Domain: von Willebrand factor type A repeat homology < VW11>
F;2633-2806/Domain: von Willebrand factor type A repeat homology < VW12>
F;307-3122/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
F;2013-0039/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
F;201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 3(VI) chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_chan;
C;Accession: A37797; A34270; A32674
R;Doliana, R.; Bonaldo, P.; Colombatti, A.
J. Cell Biol. 111, 2197-2205, 1990
A;Title: Multiple forms of chicken alpha3(VI) collagen chain A;Reference number: A37797; MUID:91035630; PMID:1977751
A;Accession: A37797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
A37797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracel F;1-25/Domain: signal sequence #status predicted <SIG> F;26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT> F;26-3137/Domain: non-collagenous #status predicted <NNC> F;36-2042/Domain: von Willebrand factor type A repeat homology <VW01> F;36-202/Domain: von Willebrand factor type A repeat homology <VW01>
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A; Residues: 2151-2199; 2792-3137 < BO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The carboxyl terminus of the chicken alpha3 chain A;Reference number: A32674; MUID:90062147; PMID:2584214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 264, 20235-20239, A; Title: The carboxyl terminus o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPARC: UPI0000173C38; GB: M24282 A; Note: the authors translated the codon TTC for residue 1916 as Leu and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Structural and functional features of the alpha3 chain indicate a bridging A;Reference number: A34270; MUID:90212613; PMID:2322559 A;Accession: A34270
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A;Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A;Cross-references: UNIPROT:P15989; UNIPARC:UP10000173C31; UNIPARC:UP10000173C32; UNIPAR
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Chem. 264, 20235-
38
                                                                                                                                                                                 Similarity
                                                                     DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
DIIFLVDSSWSIGKEHFQLVREFLYDVVKALDVGGNDFRFALVQFSGNPHTEFQLNTYPS
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                                                                                                                                          Score 216.5; DB Pred. No. 1e-10; 6; Mismatches
                                                                                                                                                                                                                DB 2;
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A;Accession: S13679
A;Accession: S13679
A;Molecule type: mRNA
A;Roelecule type: mRNA
A;Residues: 1-30, 237-313, 'CWW', 318-322, 'AR', 326-1815, 'FD', 1818-1819, 'ID', 1822-3176
A;Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:g3127925
                                                                                                                                                                 A;Cross-references: UNIPROT:P12111; UNIPARC:UPI0000126D4F; R;Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; EMBO J. 9, 385-393, 1990
                                                                                                                                                                                                                                                                                                                                                                                 collagen alpha 3(VI) chain precursor [validated] - human
N;Contains: collagen alpha 3(VI) chain, splice form A9/N10(-)
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence revision 12-Nov-1999 #text change 16-Aug-2004
C;Accession: A59140; S13679; S24465; A57083; S28776; S00Z45; C31952; C29848;
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A;Residues: 1-741 <AAA>
A;Residues: UNIPROT:Q8NDE6; UNIPARC:UPI000016ACCB; EMBL:AL137638
A;Experimental source: adult testis; clone DKFZp434J065
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Duesterhoeft, A.; Lauber, submitted to the Protein Sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein DKFZp434J065.1 - C;Species: Homo sapiens (man)
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A; Accession:
                                                                                 A;Reference number: S13679;
A;Accession: S13679
                                                                                                                                                    A; Title: Mosaic
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A; Accession: A59140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z23035
A; Accession: T46488
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C;Accession: T46488
                                                                                                                                                                                                                                 A; Residues: 1-3176 < CHU>
                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                             A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                              submitted to GenBank,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL-HFVDVDDLHIIVQELRGSI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKDMKKAV-AHMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVFRAAIVFTDGRAQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICE 621
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                                                                                                                                                    structure of
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                                                                                                          MUID:90151612;
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ce Database,
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Pred. No. 3.1e-11;
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                                                                                                          PMID:1689238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Gassenhuber,
January 2000
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                                                                                                                                                  type
                                                                                                                                                                                         GB:X52022; NID:g3127925; PIDN Kuo, H.J.; Glanville, R.; May
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 574-85;955-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',1508
A;Residues: 574-85;955-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',
A;Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
C1C; UNIPARC:UPI0000173C1D; UNIPARC:UPI0000173C1F; UNIPARC:UPI0000173C17;
I0000173C25; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C17
R;Zanussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A;Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain A;Reference number: S28776; MUID:93054780; PMID:1339440
A;Recession: A57083
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A; Accession: S28776 A;Cross-references: UNIPARC:UPI0000173C28 A; Molecule type: DNA A; Residues: 310-328 <ZAN>

A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 32-126,'AK',129-136,'L',138-236 <ZA2>
A;Residues: 32-126,'AK',129-136,'L',138-236 <ZA2>
A;Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1;
A;Cross-references: V. Dentzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, N A; Accession: S00245 A; Title: Characterization of three constituent chains of A; Reference number: S00126; MUID:88029444; PMID:3665927 R;Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, Eur. J. Biochem. 168, 309-317, 1987 collagen type VI by peptide seq Bernard, M.P.; PID:

A;Molecule type: mRNA; protein A;Residues: 2024-2046;2092-2156,'R';2203-2208,'X',2210-2211,'X',2213-2227;2228-2251;2314 A;Cross-references: UNIPARC:UPI000016A705; UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A; ID:g1335034

A;Note: the mRNA portion of the sequence corresponds to residues 2092-2157 R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Tin J. Biol. Chem. 263, 18601-18606, 1988
J. Biol. Chem. 263, 18601-18606, 1988
A;Title: Amino acid sequence of the triple-helical domain of human collager A;Reference number: A31952; MUID:89066644; PMID:3198591
A;Accession: C31952 collagen type Timpl,

A; Molecule type: mRNA A; Residues: 2038-2373 < CH4>

A,Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778 A;Note: parts of this sequence were determined by protein sequence R;Weil, D.; Mattei, M.G.; Passage, E.; Van Cong, N.; Pribula-Coman, J. Hum. Genet. 42, 435-445, 1988 Pribula-Conway, sequencing D.; Mann,

A;Title: Cloning and chromosomal localization of human genes encoding the A;Reference number: A29848; MUID:88161046; PMID:3348212 A;Accession: C29848 A;Molecule type: mRNA A;Residues: 2092-2151 <MEI>
A;Residues: 2092-2151 <MEI> three chains ō

K.; Deutzn

A;Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:g291919; A;Note: part of this sequence was determined by protein sequencing R;Jander, R.; Rautenberg, J.; Glanville, R.W.

Eur. J. Biochem. 133, 39-46, 1983
A;Title: Further characterization of the three polypeptide chains cap;Reference number: \$26506; MUID:83209648; PMID:6852033 PIDN: AAA52057.1; PID:

o F

bovine

and

human

ğ

A; Accession: S26510

A; Molecule type: protein A; Residues: 'SAIAGVAGVG' < JAN>

A;Cross-references: UNIPARC:UPI0000173C2F
A;Note: this sequence cannot be reliably placed and probably represents the results
A;Note: this sequence cannot be reliably placed and probably represents the results
A;Note: this sequence cannot be reliably placed and probably represents the results
A;Note: this sequence cannot be reliably placed and probably Pan, T.C.; Chu, M.L.; Timpl, R.

Bur. J. Blochem. 225, 573-580, 1994
A;Title: Recombinant expression and properties of the Kunitz-type protease-inhibitor
A;Reference number: S48709; MUID:95045506; PMID:7525281 from

protease-inhibitor

A; Accession: S48709

<MAY>

A;Note: engineered sequence to allow isolation of the Kunitz-type proteinase inhibitor h R;Arnoux, B.; Merigeau, K.; Saludjian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O.; submitted to the Brookhaven Protein Data Bank, August 1994 A;Molecule type: mRNA
A;Residues: 'MRAWIFFLLCLAGRALAA',3102-3176
A;Cross-references: UNIPARC:UPI0000173C30 ă

A; Contents: annotation; X-ray crystallography, 1.6 angstroms, residues 3106-3160 A; Note: engineered sequence expressed in Saccharomyces cerevisiae strain mt-663 C; Comment: Prolines and lysines at the third position of the tripeptide repeating sines are 5-hydroxylated and subsequently O-glycosylated.
C; Comment: The fibronectin type III repeat homology domain may be released during C; Genetics: domain may be released during repeating proces unit

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F;8e-307/Domain: anino-terminal nonhelical #status predicted cANH-
F;26-307/Domain: anino-terminal nonhelical #status predicted cANH-
F;26-307/Domain: von Willebrand factor type A repeat homology <WW02>
F;340-405/Domain: von Willebrand factor type A repeat homology <WW02>
F;443-608/Domain: von Willebrand factor type A repeat homology <WW02>
F;443-608/Domain: von Willebrand factor type A repeat homology <WW03>
F;337-999/Domain: von Willebrand factor type A repeat homology <WW04>
F;1835-999/Domain: von Willebrand factor type A repeat homology <WW05>
F;1027-1191/Domain: von Willebrand factor type A repeat homology <WW06>
F;1331-1394/Domain: von Willebrand factor type A repeat homology <WW06>
F;1337-1802/Domain: von Willebrand factor type A repeat homology <WW09>
F;1637-1802/Domain: von Willebrand factor type A repeat homology <WW09>
F;1637-1802/Domain: von Willebrand factor type A repeat homology <WW09>
F;1637-1802/Domain: von Willebrand factor type A repeat homology <WW09>
F;1637-1802/Domain: von Willebrand factor type A repeat homology <WW09>
F;1637-1802/Domain: von Willebrand factor type A repeat homology <WW10>
F;2040-2042/Region: cell attachment (R-G-D) motif
F;2164-2150/Region: cell attachment (R-G-D) motif
F;217-2180/Domain: von Willebrand factor type A repeat homology <WW11>
F;267-2196/Region: cell attachment (R-G-D) motif
F;267-2196/Region: cell attachment (R-G-D) motif
F;267-2196/Region: von Willebrand factor type A repeat homology <WW12>
F;267-2196/Region: cell attachment (R-G-D) motif
F;2685-2986/Region: cell attachment (R-G-D) motif
F;2697-3072/Domain: von Willebrand factor type A repeat homology <W12>
F;267-2196/Region: cell attachment (R-G-D) motif
F;2685-2986/Region: cell attachment (R-G-D) motif
F;2697-3072/Domain: von Willebrand factor type A repeat homology <W12>
F;267-2986/Region: cell attachment (R-G-D) motif
F;267-2986/Region: cell attachment (R-G-D) motif
F;2685-2986/Region: cell attachment (R-G-D) motif
F;2697-2986/Region: cell attachment (R-G-D) motif
F;2697-2986/Region: cell attachment (R
                                                                                               A;Reference number: I51027; MUID:95246925; PMID:7729585
A;Accession: I51027
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I51027
                                                                                                                                                                                                                                                                       R; Wei, Y.; Yang, E.V.; K
Dev. Biol. 168, 503-513,
A; Title: Monoclonal anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type XII collagen alpha-1 chain - eastern newt (fragment) (eastern newt) C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
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A;Description: structural component of extracellular tissue microfibrils associated with C;Superfamily: collagen VI
C;Keywords: alternative splicing; blocked amino end; cell binding; coiled coil; extrace)
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A;Status: preliminary; translated A;Molecule type: mRNA
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26-3176/Product: collagen alpha 3(VI) chain #status predicted <MATI>
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503-513, 1995
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31.4%; Pred. No. 6.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                  K.P.; Tassava, R.A.
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J. Biol. Chem. 269, 22811-22816, 1994
A;Title: The role of the I domain in ligand binding of A;Reference number: A55348; MUID:94357930; PMID:7521332
A;Scratus.
                                 J. Biol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated
A;Reference number: A45226; MUID:93155124; F
A;Accession: A45226
                                                                                                                                                             integrin alpha-1 chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994
                                                                                                                  C;Accession: A45226
R;Briesewitz, R; Epstein, M.R.; Marcantonio,
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A; Residues: 1-272 < KER >
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C;Accession: A55348
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A;Cross-references: UNIPROT:Q91145; UNIPARC:UPI0000126D2E; EMBL:U19494; NID:g632647; PII
F;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
A;Status: preliminary;
A;Molecule type: mRNA
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Best Local S
Matches 65
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                        LALVTIVEAL 240
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                    not compared with conceptual translation
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27.9%;
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Pred. No. 9.9e-10;
7; Mismatches 91
                                                            forms of the PMID:8428973
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A;Cross-references: UNIPROT:Q05707; UNIPARC:UPI00000716A9; GB:M64108; NID:g340081; PIDN:C;Reywords: glycoprotein
F;165-246/Domain: fibronectin type III repeat homology <FN3A>
F;255-338/Domain: fibronectin type III repeat homology <FN3B>
F;347-427/Domain: fibronectin type III repeat homology <FN3C>
F;347-427/Domain: fibronectin type III repeat homology <FN3C>
F;436-520/Domain: fibronectin type III repeat homology <FN3E>
F;547-632/Domain: fibronectin type III repeat homology <FN3E>
F;541-632/Domain: fibronectin type III repeat homology <FN3F>
F;641-723/Domain: fibronectin type III repeat homology <FN3F>
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A40970
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A;Cross-references: UNIPROT:P56199; UNIPARC:UPI000012D9EB
A;Experimental source: hepatoblastoma cell line HepG2
A;Note: sequence extracted from NCBI backbone (NCBIP:124326)
F;142-317/Domain: von Willebrand factor type A repeat homology <VWAl>
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R;Just, M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripier, D.; Stein, H.; Schuppan, D.
J. Biol. Chem. 266, 17326-17332, 1991
J. Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular A;Reference number: A40970; MUID:91373351; PMID:1716629
A;Accession: A40970
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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Search completed: February 13, 2006, 07:49:17 Job time: 27.7893 secs
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A; Residues: 1-843 < JUS>
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                                                                                                   DSTHVYNVAEFDLMHTVVESL 143
                                                                                                                                                                                                       KPEAGSRTGVSKIGILITDGKSQDDIIPPSRNLRESGVELFAIGVKNADVNELQEIASEP
                                                                                                                                                                                                                                                      AEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAP 154
                                                                                                                                                                                                                                                                                                       VGSEKTRIGLAQYSGDPRIEWHLNAFSTKDEVIEAVRNLPYKGGNTLTGLALNYIFENSF
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32.6%; Pred. No. 3.7e-09;
ative 26; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                           68;
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Maximum DB
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Perfect score:
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-MODEL=frame+ nzp.query.fasta 1
-QEV=xlp
-B=Published Applications AA New -OFMT=fastan -SUFFIX=Tapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
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-MODEL=frame+_n2p.model
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-11-186-284-26

US-11-169-041-160

US-10-131-826A-294

US-11-113-424-39

US-11-113-449-6

US-11-192-449-5

US-11-192-449-5

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US-10-453-372-2
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equence 921, Applequence 8, Applequence 7, Applequence 2, Applequence 4, Applequence 4, Applequence 2, Appleque	1111	equence 22, equence 21, equence 25, equence 4, P equence 6, P	200, Ap 202, Ap 204, Ap 206, Ap 182, Ap 1184, App 118, App 24, App	Sequence 34, Appli Sequence 4, Appli Sequence 186, App Sequence 180, App Sequence 194, App Sequence 178, App Sequence 196, App

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/9823187
PRIOR APPLICATION NUMBER: 60/9823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR RILING DATE: 2000-03-10
PRIOR RILING DATE: 2000-03-19
PRIOR RAPPLICATION NUMBER: 60/195792
PRIOR RAPPLICATION NUMBER: 60/195792
PRIOR RAPPLICATION NUMBER: 09/839446
PRIOR RAPPLICATION NUMBER: 09/83946
PRIOR RAPPLICATION NUMBER: 09/863776
PRIOR RAPPLICATION NUMBER: 09/939398
PRIOR RILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR RILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR RAPPLICATION NUMBER: 09/939398
PRIOR RAPPLICATION NUMBER: 09/939398
PRIOR RAPPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-05-31
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITS
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029PRNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/11/186,284
PRIOR APPLICATION NUMBER: US/11/186,284
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; ORGANISM: Homo s
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                                                                                                                                                                     APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
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; Publication No. US200;
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SEQ ID NO 26
FUGTH: 3063
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PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
                      APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NUMBER: US/11/169,041
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PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: PatentIn version 3.2
SEQ ID NO 160
LENGTH: 517
; TYPE: PRT
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                                                          APPLICANT:
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                                        APPLICANT
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059388
PRIOR FILING DATE: 1997-09-19
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PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
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LENGTH: 915
TYPE: PRT
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
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                                      LeuArgGluAsnValProArgValIleMetIleValThrAspGlyArgProGlnAspSer 176
                                                                                                                LysSerGluValGluArgAlaValLysArgMetArgHisLeuSerThrGlyThrMetThr
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Publication No. US20050260713A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 956
TYPE: PRT
ORGANISM: Homo
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CURRENT FILING DATE: 2005-04-21
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APPLICATION NUMBER: 60/315,617
FILING DATE: 2001-08-29
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FILING DATE: 2001-05-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/307,506 FILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-12-20
APPLICATION NUMBER: 60/311,613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-05-29
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                                                                                        GlyLeuLeuGlnTyrGlySerThrValLysAsnGluPheSerLeuLysThrPheLysArg
                                                                                                                                                                LysGluPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal
                                                                                                                                                                                                                                         AspLeuValPheIleIleAspSerSerArgSerValAsnThrHisAspTyrAlaLysVal
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PRIOR APPLICATION NUMBER: 10/061,658

PRIOR FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 09/557,092

PRIOR FILING DATE: 2000-04-21

PRIOR FILING DATE: 1999-04-22

PRIOR FILING DATE: 1999-04-22
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Publication No. US20050281818A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version SEQ ID NO \boldsymbol{6}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment
FILE REFERENCE: A073-USCN3
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APPLICANT: Gotwall
APPLICANT: Koteli
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GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGT----GACACCCAC
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                                  GlyIleValGlnTyrGlyGluAsnValThrHisGluPheAsnLeuAsnLysTyrSerSer
                                                                                                            ThrAlaPheLeuAsnAspLeuLeuLysArgMetAspIleGlyProLysGlnThrGlnVal 59
                                                                                                                                                                                   AspIleValIleValLeuAspGlySerAsnSerIle-----TyrProTrpAspSerVal
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RESULT 7

US-11-192-449-9

Sequence 9, Application US/11192449

Publication No. US20050281818A1

GENERAL INFORMATION:

APPLICANT: Biogen, Inc.

APPLICANT: Gotwals, Philip

APPLICANT: Gotwals, Philip
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Query Match:
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                                                                                                                                                                                                                                                                                                                                             US-11-192-449-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
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TITLE OF INVENTION: Method for the Treatment of Fibrosis
FILE REFERENCE: A073-USCN3
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/137,214
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                                                         AspIleValIleValLeuAspGlySerAsnSerIle-----TyrProTrpAspSerVal
                                                                                               GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
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US-11-192-449-5
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                                                            Query Match:
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US-11-192-449-5
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  US-10-699-035A-1 (1-537) x US-11-192-449-5 (1-214)
                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                          Pred. No.:
                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILLING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILLING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR FILLING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILLING DATE: 1999-04-22
PRIOR FILLING DATE: 1999-04-22
PRIOR FILLING DATE: 1999-04-22
                                                                                                                                                                                                                                                                               SOFTWARE: FABLSEQ SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/11192449
Publication No. US20050281818A1
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gotwals, Philip
APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment
FILE REFERENCE: A073-USCN3
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/137,214 PRIOR FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                         LENGTH: 21
TYPE: PRT
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Matches:
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Indels:
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Prior Application removed - See Palm or File Wrapper;
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 34
LENGTH: 678
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-703-34
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US-10-063-703-34
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 Percent Similarity:
Best Local Similarity:
                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/063,703
CURRENT FILING DATE: 2002-05-08
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Matches:
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                       Alignment Scores:
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US-11-102-240-34
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   Pred.
                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/11102240 Publication No. US20050260647A1
                                                                                                                SEQ ID NO 34
LENGTH: 678
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                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS' TITLE OF INVENTION: ESOPHAGEAL TUMOR FILE REFERENCE: P3230R1C106C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
                                                                                                                                                     PRIOR FILING DATE: 199-12
NUMBER OF SEQ ID NOS: 170
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                                                                           TYPE: PRT
ORGANISM: Homo
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Wood, William I
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Grimaldi, Christopher J.
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Percent Similarity:
Best Local Similarity:
Query Match:
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                    Score:
                                         Pred. No.:
                                                          Alignment Scores
                                                                                                                                                                                                                                      TITLE OF INVENTION: MODIFIED POLYPEPTIDES ST
TITLE OF INVENTION: DESIRED CONFORMATION AN
FILE REFERENCE: CFBF-P02-021
CURRENT APPLICATION NUMBER: US/11/080,026
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 09/945,265
PRIOR APPLICATION NUMBER: 09/945,265
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,700
PRIOR FILING DATE: 2000-09-01
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Percent Similarity:
                                                                                                    US-11-080-026-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/11080026 Publication No. US20050260192A1 GENERAL INFORMATION:
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Springer, Timothy A. APPLICANT: Shimaoka, Motomu APPLICANT: Lu, Chafen
                                                                                                                   TYPE: PRT
ORGANISM: Homo
                                                                                                                                                          LENGTH: 1152
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Query Match:
DB:
                                                  CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/78939
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2001-02-23
PRIOR PPLICATION NUMBER: 60/185967
PRIOR PPLICATION NUMBER: 99/823187
PRIOR APPLICATION NUMBER: 09/823187
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 09/839446
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2000-03-25
PRIOR PILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR APPLICATION NUMBER: 09/863776
PRIOR APPLICATION NUMBER: 09/863776
PRIOR APPLICATION NUMBER: 09/863776
PRIOR PILING DATE: 2001-05-23
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  PRIOR PRIOR PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 21402-589 A
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APPLICATION NUMBER: 60/208263 FILING DATE: 2000-05-31 APPLICATION NUMBER: 09/939398
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APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NU
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR APPLICATION NUMBER: 60/185967
PRIOR APPLICATION NUMBER: 60/9823187
                                                                                                                                                                                                                          RESULT 13
US-10-453-372-180
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PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CURASeqList version 0.1
SEQ ID NO 186
LENGTH: 709
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                        Sequence 180, Application US/10453372 Publication No. US20060003323A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
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LENGTH: 709
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PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
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PRIOR FILING DATE: 2000-03-25
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TYPE: PRT
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 194
LENGTH: 3568
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOI
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APPLICATION NUMBER: 09/939398
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APPLICATION NUMBER: 09/863776
FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/823187
FILING DATE: 2001-03-29
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FILING DATE: 2000-03-10
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  SerAsnGlyGlyAspPro---ArgProIleAlaAlaSerLeuArgAspSerGlyValGlu
                                     TCCAGC-----GACCCTGTGGGGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACC 396
                                                                                                                     GAAGCATCAGGTGCCCGGCCAGGGGTGCCCCAAAGTGCTGGTGGTGGCTGACAGATGGCGGC
                                                                                                                                                                                         CGCATGGGTGACACCCACACTGGCCTGGCCTGGTCTATGCCAAGGAACAGCTGTTTGCT
                                                                                                                                                                                                                                      ArgArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIleProAlaIleSerTyr
                                                                                                                                                                                                                                                                             GGTGAGGCTGCCCAG------GATGCGGTGCGTGCTTCTGCCCAG
                                                                                                                                                                                                                                                                                                                  AlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIleSerThr
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                                                                            -----HisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyr 195
                                                                                                                                                          ArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeu---
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PRIOR FILING DATE: 2001-02-23
PRIOR PPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-19
PRIOR PPLICATION NUMBER: 09/939446
PRIOR PPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
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Publication No. US20060003323A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1609
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PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
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                                                                                                                     124 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG 183
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                                         GGTGAGGCTGCCCAG-----
ArgArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIleProAlaIleSerTyr 159
                                                                            AlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIleSerThr 139
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Result
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

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Copyright (c) 1993 - 2006 Biocceleration
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US-11-186-284-26
US-11-189-041-160
US-11-113-424-39
US-11-192-449-9
US-11-192-449-9
US-11-192-449-9
US-11-192-440-34
US-11-192-40-34
US-11-063-703-34
US-11-063-372-186
US-10-453-372-186
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US-10-453-372-206
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Sequence 2, Appli
Sequence 26, Appl
Sequence 294, App
Sequence 39, Appl
Sequence 9, Appli
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Sequence 34, Appli
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Sequence 19, Appl		w	•	•	•	-	Sequence 21, Appl	Sequence 38, Appl	•	Sequence 38, Appl	Sequence 38, Appl	Sequence 38, Appl	•	Sequence 628, App	Sequence 625, App				

ALIGNMENTS

; ORGANISM: Homo sapiens US-10-453-372-2 PRIOR APPLICATION NUMBER: 09/839446 PRIOR FILING DATE: 2001-03-19 PRIOR APPLICATION NUMBER: 60/199476 PRIOR FILING DATE: 2000-03-25 PRIOR APPLICATION NUMBER: 09/863776 PRIOR FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: 60/208263 PRIOR FILING DATE: 2001-05-31 PRIOR APPLICATION NUMBER: 09/939398 PRIOR APPLICATION NUMBER: 09/939398 PRIOR APPLICATION NUMBER: 09/939398 PRIOR APPLICATION NUMBER: 09/939398 Remaining Prior Application da NUMBER OF SEQ ID NOS: 1609 SOFTWARE: CuraSeqList version SEQ ID NO 2 LENGTH: 445 Sequence 2, Application US/10453372 Publication No. US20060003323A1 GENERAL INFORMATION: Query Match Best Local Similarity Matches 418; Conserv TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO FILE REFERENCE: 21402-589 A CURRENT PELICATION NUMBER: US/10/453,372 CURRENT FILING DATE: 2003-06-03 FRIOR APPLICATION NUMBER: 09/789390 PRIOR APPLICATION NUMBER: 09/789390 PRIOR FILING DATE: 2001-02-23 PRIOR PILING DATE: 2001-03-01 PRIOR EPLICATION NUMBER: 60/185967 PRIOR FILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: 60/185967 PRIOR PILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: 60/195792 PRIOR PILING DATE: 2000-03-10 PRIOR PILING PILING DATE: 2000-03-10 PRIOR PILING PI PRIOR APPLICATION NUMBER: 60/227800 PRIOR FILING DATE: 2000-08-25 APPLICANT: Alsobrook, et al. TYPE: PRT MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL Conservative 98.9%; data removed -0 Score 2130.5; DB 6; Pred. No. 3.9e-161; 0; Mismatches 0; See File Wrapper or Indels Length 445; 27; Gaps

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VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA 120 MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL

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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE-
FILE REFERENCE: MPMO1-02992RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR APPLICATION NUMBER: US/0/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-20
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-26
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                                                                                                                                                       Query Match
Best Local
                                                                                                                                      Matches
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KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF
                                                                                    RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLFLGTGALRASLVHVGSRPYTEFFFGQH
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                                                                                                                                      Conservative
                                                                                                                                  19.6%; Score 421.5; DB 7; 27.5%; Pred. No. 5.5e-25; tive 59; Mismatches 174;
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; ORGANISM: Homo
US-11-169-041-160
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US-11-169-041-160
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TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF

TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE

TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER

TITLE REFERENCE: 10001 NP

CURRENT APPLICATION NUMBER: US/11/169,041

CURRENT FILING DATE: 2005-06-28

PRIOR APPLICATION NUMBER: 60/584,405

PRIOR FILING DATE: 2004-06-30

NUMBER: OF SEQ ID NOS: 527

SOFTWARE: Patentin version 3.2

SEQ ID NO 160

LENGTH: 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 160, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                  y Match 18.6%; Score 401; DB 7; Local Similarity 30.0%; Pred. No. 2.2e-24;
                                                                                                                                                                                                                                                                                                         143
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                                         ----PGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHAR 317
                                                                                                                --LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQL 261
                                                                                                                                                       IKLRNSDVEIFAVGVKDAVDSELEAIASPPAETHVFTVEDFDAFQRISFELTQSICLRIE
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     TVVEPASSTSVVLNSLKPETLYLVNVTAEYEDGFSIPLAGEETTEEVKGAPRNLKVTDET
                                                                              QELAAIKKKAYVPPKDLSFSEVTSYGFKTNWSPAGENVFSYHI----TYKEAAGDDEV
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                                                                                                                                                                                                                                                                                                                                                                                   61; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 517;
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                                                                                                                                                                                                 SEQ ID NO 294
LENGTH: 915
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APPLICANT:
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PRION FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                         TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                      FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-09-18 APPLICATION NUMBER: 60/059352
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/059122
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APPLICATION NUMBER: 60/059117
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                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/059588
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/059184
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45
                                  16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                                                       Similarity
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ALLESSCEN-----KRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGL
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DeForge, Laura
Desnoyers, Luc
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                                                                                       11.8%;
                                                                      36;
                                                                  Score 253.5; Db 6;
Pred. No. 2.1e-12;
                                                                                                          Length 915;
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SEQ ID NO 39
LENGTH: 956
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Publication No. US20050260713A1
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TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
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CURRENT FILING DATE: 2005-04-21
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PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                    Local
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FILING DATE: 2001-08-29
APPLICATION NUMBER: 60/307,506
FILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-09-14
APPLICATION NUMBER: 60/294,075
FILING DATE: 2001-05-29
APPLICATION NUMBER: 60/288,153
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219 VANFSQIETLTSVFQK 234
                                       191 --HFVDVDDLHIIVQE
                                                                              159
                                                                                                                134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL--
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                                                                                                                                                       99 LQYGSTVKNEFSLKTFKRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLR 158
                                                                                                                                                                                            76 VHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP--
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                                                                              ENVPRVIMIVIDGRPQDSVAEVAAKARDIGILIFAIGVGQVDFNTLKSIGSEPHEDHVFL
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                                                                                                                                                                                                                                                                                                                 11.8%; Score 253.5; DB 7
31.6%; Pred. No. 2.2e-12;
tive 36; Mismatches 85
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RESULT 6 US-11-192-449-6

; Sequence 6, Application US/11192449

Gaps

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APPLICANT: Gotwals, Philip
APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment of Fibrosis
FILE REFERENCE: A073-USCN3
CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 69/130,847
PRIOR APPLICATION NUMBER: 60/137,214
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US-11-192-449-9
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PRIOR FILING DATE: 2003-07-22
PRIOR PELICATION NUMBER: 10/061,658
PRIOR PELICATION NUMBER: 10/061,658
PRIOR PELICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/137,214
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Best Local Similarity
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LENGTH: 214
SEQ ID
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  SOFTWARE:
                                                  NUMBER OF SEQ ID NOS:
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NUMBER OF SEQ ID NOS: 10
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TITLE OF INVENTION: Method for the Treatment of Fibrosis
FILE REFERENCE: A073-USCN3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 DIVIVLDGSNSI--YPWDSVTAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSS
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                         FastSEQ for Windows Version 4.0
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; ORGANISM: Rat
US-11-192-449-5
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PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 69/130,847
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Matches
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SEQ ID NO 5
LENGTH: 214
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APPLICANT: Biogen, Inc.
APPLICANT: Gotwals, Pt
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Best Local Similarity
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TYPE: PRT
ORGANISM:
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CURRENT FILING DATE: 2005-07-28
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TITLE OF INVENTION: Method for the Treatment
FILE REFERENCE: A073-USCN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/137,214
PRIOR FILING DATE: 1999-06-01
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                                               140 LKQVIQDCEDENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEK--HFFNVSDELA 197
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                                                                                                                                            TEEVLVAAKKIGRQGGLQTMTALGIDTARKEAFTEARGARRGVKKVMVIVTDGESHDNYR 139
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                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 185; DB 7
31.9%; Pred. No. 8e-08;
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                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 214;
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; ORGANISM: Homo Sapien
US-10-063-703-34
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                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/11102240 Publication No. US20050260647A1 GENERAL INFORMATION:
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Best Local
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APPLICANT:
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul L.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul L.
APPLICANT: Godowski, Paul L.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANTON NUMBER: US/11/102,240
CURRENT APPLICATION NUMBER: 10/06362
PRIOR APPLICATION NUMBER: 10/06367
PRIOR APPLICATION NUMBER: 10/06867
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2000-08-24
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CURRENT FILING DATE: 2002-05-08
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Pred. No. 4.4e-07;
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; PRIOR APPLICATION NUMBER: 60/1
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 34
; LENGTH: 678
; TYPE: PRT
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                                                                                    ; ORGANISM: Homo US-10-453-372-186
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                                                                                                                                                                  Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 186
                 Query Match
Best Local Similarity
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO-
FILE REFERENCE: 21402-589 A
                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
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CURRENT FILING DATE: 2003-06-03
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PRIOR APPLICATION NUMBER: 09/939398
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PRIOR APPLICATION NUMBER: 09/863776
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                                                                                                                        TYPE: PRT
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                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVD-VDDLHIIVQELRGSILDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             555 KPDILNAIKRVGYWSGGTSTGAAINFALEQLFKK---SKPNKRKLMILITDGRSYDDVRI
                                                                                                                                                  709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARFGVFKVLVWVTDGGSSDFVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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    Conservative
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8.1%; Score 175; DB 6;
29.3%; Pred. No. 2.4e-06;
ative 34; Mismatches 94
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    See File Wrapper or

                                        Length 709;
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    Indels
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US-10-453-372-180
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LENGTH: 709
TYPE: PRT
ORGANISM: Homo s
JS-10-453-372-180
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Best Local (
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CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
FILE REFERENCE: 21402-589 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
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    178
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                                                                                                                               101 VPTATRVAIVTFSSKNYVVPRVDYISTRRARQHKCALLLQEIPÄISYRGGGTYTKGÄFQQ 160
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                                                                                                                                                                       67 GTGALRASLVHVGSRPYTEFPFGQHSSGEAAQ-----DAVRASAQRMGDTHTGLALVY 119
                                                                                                                                                                                                                 49
                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                           7 LGLALSURLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPL
                                                                                                                                                                                                                                                                                                                        Similarity
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  LSAAASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGF 228
                                              AAQILL----HARENSTKVVFLITDGYSNGGDP-RPIAASLRDSGVEIFTFGIWQGNIRE
                                                                                   AKEQLFAEASGARPGVPKVLVWVTDGGSS--DPVGPPMQELKDLGVTVFIVSTGRGNFLE
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o. US20060003323A1
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29.4%; Pred. No. 2.9e-06;
tive 33; Mismatches 96;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                          Length 709;
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Best Local Similarity
Thes 74; Conserve
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US-11-080-026-4
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US-10-453-372-182
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PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR HILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/839446
                                                                                                                                                                                                                                                                                                  Sequence 182, Application US/10 Publication No. US20060003323A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1152
TYPE: PRT
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APPLICANT: Springer, Timothy A.
APPLICANT: Shimaoka, Motomu
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IITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A

TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR

FILE REFERENCE: CFBF-P02-021

CURRENT APPLICATION NUMBER: US/11/080,026

CURRENT FILING DATE: 2005-03-15

PRIOR APPLICATION NUMBER: 09/945,265

PRIOR APPLICATION NUMBER: 09/945,265

PRIOR FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: US 60/229,700

PRIOR APPLICATION NUMBER: US 60/229,700

PRIOR APPLICATION DATE: 2000-09-01

NUMBER: OF SEQ ID NOS: 4
                                                                                                                                                                                                              TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, FILE REFERENCE: 21402-589 A CURRENT APPLICATION NUMBER: US/10/453,372
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                                                                                                                                                                                             CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                   APPLICANT: Alsobrook, et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 ALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLF--SLMQYSEEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 TEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 -- RG-----DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQKFPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGGS-SDPVG--PPMQELKDLGVTVFIVSTG-----RGNFLELSAAASAPAEKHLHFV-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEALKTIONOLREKIF-AIEGTOTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSY
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                                                                                                                                                                                                                                                                                                                                              Application US/10453372
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25.0%; Pred. No. 5.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LHSFEE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122;
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139

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194 257

AND METHOD

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US-10-601-368-18
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; ORGANISM: Homo sapiens
US-10-601-368-18
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                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PAIM.

NUMBER OF SEQ ID NOS: 1609

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 182

LENGTH: 709

TYPE: PRT

ORGANISM: Homo sapiens
                                                                                                                                                   Query Match 8.0%; Score 172.5; DB 6; Length 1167; Best Local Similarity 24.0%; Pred. No. 7.3e-06; Matches 90; Conservative 47; Mismatches 119; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/10601368 Publication No. US20050260702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.0%; Score 173; DB 6; Length 709; Best Local Similarity 29.4%; Pred. No. 3.5e-06; Matches 68; Conservative 33; Mismatches 96; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/9/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
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PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pan, Yang
APPLICANT: LOYA, JOSE M.
TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/227800 PRIOR FILING DATE: 2000-08-25.
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FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 LNDMASTPKEEHCYL-----LHSFEE-----FEALARRALH-EDLPSGSF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 LSAAASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGF 228
                                                143 ARVDASFQPQGSLAPTAQRCPTYMDVVIVLDGSNSI--YPWSEVQTFLRRLVGKLFIDPE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 AAQILL----HARENSTKVVSLITDGYSNGGDP-RPIAASLRDSGVEIFTFGIWQGNIRE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 VPTATRVAIVTFSSKNYVVPRVDYISTRRARQHKCALLLQEIPAISYRGGGTYTKGAFQQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AKEQLFAEASGARPGVPKVLVWVTDGGSS--DPVGPPMQELKDLGVTVFIVSTGRGNFLE 177
     70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
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ALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMG-DTHTGLALVYAKEQLFAEA 128
                                                                                ARSGAERGPPAS-APRG-----DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTG 69
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429	274 404	224 366	177 313	129 261	201
333 AALIGINVEEPIKGG 347 	274 DPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPAL-GSA 332	224 TSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQLPGNATDWIWAGL 273	177ELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEI 223 :	129 SGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFL 176	::

Search completed: February 13, 2006, 13:12:59 Job time: 10.087 secs

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Minimum DB
Maximum DB
                                                                                                                                                                          Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
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913
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        8 7 6 5 4 3 2 1
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                                                                                                                                                                        Published Applications AA New:
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Copyright (c) 1993 - 2006 Biocceleration Ltd
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	₅	4	ω	2	_	Result No.
149.5	150.5	156	161	162	162	162	162	162	162	162	162	162	162.5	163	183	183	185	194	194	251.5	251.5	257.5	263.5	913	Score
16.4	16.5	17.1	17.6	17.7			17.7	17.7	17.7	17.7	17.7	17.7	17.8	17.9	20.0	20.0	20.3	21.2	21.2	27.5	27.5	28.2	28.9	100.0	Query
182	1167	709	709	3570	3570	3570	3570	3570	3570	3570	3568	709	1152	709	678	678	214	214	214	956	915	517	3063	445	Query Match Length
6	6	σ	σ	σ	6	σ	σ	6	6	6	6	თ	7	σ	7	σ	7	7	7	7	σ	7	7	σ	BB
US-10-601-368-25	US-10-601-368-18	US-10-453-372-184	US-10-453-372-182	US-10-453-372-206	US-10-453-372-204	US-10-453-372-202	US-10-453-372-200	US-10-453-372-198	US-10-453-372-196	US-10-453-372-178	US-10-453-372-194	US-10-453-372-180	US-11-080-026-4	US-10-453-372-186	US-11-102-240-34	US-10-063-703-34	US-11-192-449-5	US-11-192-449-9	US-11-192-449-6	US-11-113-424-39	US-10-131-826A-294	US-11-169-041-160	US-11-186-284-26	US-10-453-372-2	ID
Sequence 25, Appl	Sequence 18, Appl	184,	Sequence 182, App	206,	Sequence 204, App	202,		-	Sequence 196, App	e 178,	194,	18	4.	18	34,	34	5	9	6	Sequence 39, Appl	e 294,	160,	26	Sequence 2, Appli	Description

5	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	ċ
128	131	133	133	133	133.5	133.5	144.5	144.5	144.5	144.5	144.5	144.5	144.5	144.5	144.5	145.5	149.5	149.5	11000
14.0	14.3	14.6	14.6	14.6	14.6	14.6	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.9	16.4	16.4	10.1
1167	184	1170	1170	184	1196	1179	2919	2813	2764	1188	1188	1188	1166	1141	182	1147	1188	1166	1
7	σ	7	7	σ	9	7	σ	σ	σ	7	7	σ	σ	σ	σ	σ	σ	6	<
US-11-097-125-2	US-10-665-658-8	US-11-107-028-4	US-11-080-026-2	US-10-665-658-7	US-10-995-561-921	US-11-097-125-1	US-10-821-234-1133	US-10-995-561-688	US-10-995-561-691	US-11-000-463-810	US-11-000-463-338	US-10-601-368-3	US-10-601-368-4	US-10-601-368-6	US-10-601-368-7	US-10-453-372-4	US-10-601-368-21	US-10-601-368-22	
Sequence 2, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 921, App	Sequence 1, Appli	Sequence 1133, Ap	Sequence 688, App	Sequence 691, App	Sequence 810, App	Sequence 338, App	Sequence 3, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 4, Appli	Sequence 21, Appl	Sequence 22, Appl	- 4.4

ALIGNMENTS

RESULT 1 US-10-453-372-2

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                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-10-453-372-2
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PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2001-03-29
PRIOR PPLICATION NUMBER: 09/823187
PRIOR APPLICATION NUMBER: 60/195792
PRIOR APPLICATION NUMBER: 09/839446
PRIOR APPLICATION NUMBER: 09/839446
PRIOR APPLICATION NUMBER: 09/839476
PRIOR APPLICATION NUMBER: 60/199476
PRIOR APPLICATION NUMBER: 60/29476
PRIOR APPLICATION NUMBER: 60/29476
PRIOR APPLICATION NUMBER: 09/83776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR PILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/208263
PRIOR APPLICATION NUMBER: 60/208263
PRIOR APPLICATION NUMBER: 60/208263
PRIOR APPLICATION NUMBER: 60/208263
PRIOR APPLICATION NUMBER: 60/227800
PRIOR APPLICATION NUMBER: 60/227800
PRIOR PILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 2
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 180; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10453372 Publication No. US20060003323A1 GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-589 A CURRENT APPLICATION NUMBER: US/10/453,372 CURRENT FILING DATE: 2003-06-03
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
  61
                                                          32
                                                                                                                                                                                                                                                                                                                                                                      445
                                                    SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
                                                                                                                                                                   100.0%; Score 913; DB 6; Length 445; ilarity 100.0%; Pred. No. 1.4e-83; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         <u>.</u>.
                                                                                                                                                                         Gaps
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US-11-169-041-160; Sequence 160, Ap.; Publication No.
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US-11-186-284-26
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                                                                                                                                                                                                                                               RESULT 3
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                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEO ID NOS: 228
TITLE OF INVENTION: KINASES AND/OR PROTE
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
                                                                                                   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3063
                                                                                                                                                                                                                                                                                                                                                                                          498
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                                                                                                                                                                                                                                                                                                          558 RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVEDFDAFQRISFELTQSI 616
                                                                                                                                                                                                                                                                                                                                                  121 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF
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Schlegel, Robert
Monahan, John E.
                                                                                                                                                                                 Application US/11169041 b. US20060019284A1
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                                                             KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.9%; Score 263.5; 35.8%; Pred. No. 1.1e tive 30; Mismatches
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1.1e-17;
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PRIOR FILING DATE: 2004-66-30
NUMBER OF SEQ ID NOS: 527
SOPTWARE: PatentIn version 3.2
SEQ ID NO 160
LENGTH: 517
TYPE: PRT
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                                                           PRIOR PRIOR
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                                                                                                   PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
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                                                             APPLICATION NUMBER: 60/059263 FILING DATE: 1997-09-18
                       FILING DATE:
                                          APPLICATION NUMBER: 60/059352
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Watanabe, Colin K
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Stewart, Timothy A.
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 294
LENGTH: 915
TYPE: PRT
                                                                                                                                                       Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                              SEQ ID NO 39
LENGTH: 956
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Best Local &
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PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gangolli et al. TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding FILE REFERENCE: 21402-225
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
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PRIOR FILING DATE: 2000-12-19
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CURRENT FILING DATE: 2005-04-21
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/311,590
                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Homo sapiens
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FILING DATE: 2001-09-14
APPLICATION NUMBER: 60/294,075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/315,617
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    115
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KRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQ 174
                                    SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP---GVPKVLVWVTDGGSS 117
                                                                                                                RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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                                                                           RADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTF 114
                                                                                                                                                         Conservative
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                                                                                                                                                                       27.5%; Score 251.5; DB 7 32.2%; Pred. No. 3.7e-17;
                                                                                                                                                         36; Mismatches
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                                                                                                                                                                                            DB 7;
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RESULT 7
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APPLICANT: Biogen, Inc.
APPLICANT: Gotwals, Philip
APPLICANT: Gotwals, Philip
APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment of
FILE REFERENCE: A073-USCN3
CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR PILING DATE: 2003-07-22
PRIOR FILING DATE: 2003-07-22
PRIOR FILING DATE: 2003-07-21
PRIOR FILING DATE: 2003-07-01
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PRIOR FILING DATE: 2003-07-22
PRIOR PRILING DATE: 2002-02-01
PRIOR FILING DATE: 2002-02-01
PRIOR PELLOATION NUMBER: 09/557,092
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/137,214
PRIOR APPLICATION NUMBER: 60/137,214
PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                      Sequence 9, Application US/11192449
Publication No. US20050281818A1
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                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Koteliansky, Victor TITLE OF INVENTION: Method for the Treatment FILE REFERENCE: A073-USCN3 CURRENT APPLICATION NUMBER: US/11/192,449 CURRENT FILING DATE: 2005-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Biogen, APPLICANT: Gotwal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 214
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 LKKVIQDCEDENIQRFSIAILGSYNRGNLSTEKFVEEIKSIASEPTEK--HFFNVSDELA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 DIVIVLDGSNSI--YPWDSVTAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEAAQDAVRASAQRMG-DTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSD--P 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gotwals,
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Philip
Vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.2%; Score 194; DB 7;
33.5%; Pred. No. 2.7e-12;
tive 28; Mismatches 77
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                                                                                                                                                                          of Fibrosis
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LENGTH: 214
; TYPE: PRT
; ORGANISM: Rat
US-11-192-449-5
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US-11-192-449-5
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TYPE: PRT
ORGANISM: Homo sapien
US-11-192-449-9
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/61,658
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/137,214
PRIOR APPLICATION NUMBER: 60/137,214
                                                                                  Matches
                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                      SEQ ID NO 5
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Best Local
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                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Biogen,
APPLICANT: Gotwal
APPLICANT: Koteli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Koteliansky, Victor TITLE OF INVENTION: Method for the Treatment FILE REFERENCE: A073-USCN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/137,214
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEO ID NOS: 10
SOFTWARE: FastSEQ for Windows Version
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PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 TEEVLVAAKKIVORGGROTMTALGTDTARKEAFTEARGARRGVKKVMVIVTDGESHDNHR
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                                      DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIVIVILDGSNSI--YPWDSVTAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVTIVKTL 205
DIVIVLDGSNSI--YPWESVIAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gotwals, Philip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inc.
                                                                                                   20.3%;
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33.5%; Pred. No. 2.7e-12;
tive 28; Mismatches 77
                                                                             Score 185; DB 7; Length 214; Pred. No. 2.1e-11; 32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                       Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Fibrosis
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RESULT 10
US-11-102-240-34
; Sequence 34, Application US/11102240
; Publication No. US20050260647A1
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US-10-063-703-34
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CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 34
                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
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Best Local Similarity
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APPLICANT:
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                    FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
                                                                                 APPLICANT: WOOD, WISTIN L.

APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS TITLE OF INVENTION: ESOPHAGEAL TUMOR
                                                                                                                                                                    APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Eaton, Dan L. APPLICANT: Filvaroff, E
PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                           612 PAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 KPDILNAIKRVGYWSGGTSTGAAINFALEQLFKK---SKPNKRKLMILITDGRSYDDVRI 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 DIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSS 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVD-VDDLHIIVQEL 174
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Gerritsen, Mary E.
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Grimaldi, Christopher J.
Gurney, Austin L.
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Pred. No. 1.6e-10;
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US-10-453-372-186
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                                                               ; SOFTWARE: CuraSeqList v
SEQ ID NO 186
; LENGTH: 709
; TYPE: PRT
; ORGANISM: Homo sapiene
US-10-453-372-186
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US-11-102-240-34
   Query Match
Best Local S
Matches 54
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Best Local Similarity
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SEQ ID NO 34
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                                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1609
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
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APPLICATION NUMBER: 60/195792
FILING DATE: 2000-03-10
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APPLICATION NUMBER: 10/006867
FILING DATE: 2001-12-06
                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/939398
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   l Similarity
54; Conserv
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    Conservative
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17.9%; Score 163; DB 6; Length 709; 31.4%; Pred. No. 1.7e-08; tive 27; Mismatches 75; Indels
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US-10-453-372-180
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                   GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPBUTIC POLYPEPTIDES,
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
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SEQ ID NO 4
LENGTH: 1152
TYPE: PRT
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APPLICANT: Shimaoka, Motomu
APPLICANT: Lu, Chafen
TITLE OF INVENTION: MODIFIED POLYPEPTIDES
TITLE OF INVENTION: DESIRED CONFORMATION
FILE REFERENCE: CFBF-P02-021
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PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,700
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 4
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CURRENT FILING DATE: 2005-03-15
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APPLICATION NUMBER: 60/185967
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o. US20060003323A1
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SOFTWARE: CuraSeqList version 0.1
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                              APPLICATION NUMBER: 60/208263
FILING DATE: 2000-05-31
APPLICATION NUMBER: 09/939398
FILING DATE: 2001-08-24
                                                                                                                                 FILING DATE: 2001-03-19
APPLICATION NUMBER: 60/199476
FILING DATE: 2000-03-25
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                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/185967 FILING DATE: 2000-03-01
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FILING DATE: 2000-05-31
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APPLICATION NUMBER: 09/839446
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APPLICATION NUMBER: 60/195792
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APPLICATION
FILING DATE
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US-10-453-372-194
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 194
LENGTH: 3568
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                                                                                                                                                                                         SEQ ID NO 178
LENGTH: 3570
                                                                     Matches
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PRIOR FILING DATE: 2000-03-25
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-Q=/abss/ABSSWEB spool/US10699035/runat 13022006 062453 25634/app query.fasta 1
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-DB=Published Applications AA New -OFMT=fastan -SUFFIX=rapbn -MINWATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR MAX=100
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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US-10-453-372-206 US-11-149-003-16 US-10-453-372-182 US-11-182-016-31 US-11-182-016-31 US-10-453-372-180 US-10-453-372-186	-11-129-10 -10-453-37 -10-453-37 -10-453-37 -10-453-37 -10-453-37	11-192-449-6 11-192-449-9 11-182-016-2 10-821-234-1 11-182-016-2 11-182-016-2	-10-821-234-964 -111-186-284-33 -11-182-016-21 -11-182-016-21 -11-182-016-21 -10-995-561-998 -10-995-561-999	US-11-000-463-243 US-11-186-284-28 US-11-021-603-2 US-10-821-234-1096 US-11-000-463-243 US-11-186-284-28 US-11-021-603-2 US-10-821-234-1096
e 182, e 182, e 180, e 186,	e 196, Appe 178, Appe 178, Appe 198, Appe 200,	231420	equence 964, pequence 33, Appequence 21, Appequence 33, Appequence 21, Appequence 988, pequence 988, pequence 989, pequence 989, pequence 989, pequence 981,	Sequence 243, Appl Sequence 28, Appli Sequence 2, Appli Sequence 1096, Ap Sequence 243, App Sequence 28, Appli Sequence 2, Appli Sequence 2, Appli

ALIGNMENTS

US-10-453-372-2

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Sequence 2, Application US/10453372
Publication No. US2006000323A1
GENERAL INFORMATION:
APPLICAVT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
FILE REPERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT PILING DATE: 2001-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR APPLICATION NUMBER: 09/789390
PRIOR APPLICATION NUMBER: 09/823187
PRIOR APPLICATION NUMBER: 09/823187
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/823187
PRIOR APPLICATION NUMBER: 09/83776
PRIOR APPLICATION NUMBER: 09/83776
PRIOR APPLICATION NUMBER: 09/83776
PRIOR APPLICATION NUMBER: 09/83776
PRIOR APPLICATION NUMBER: 09/23893
PRIOR APPLICATION NUMBER: 09/83776
PRIOR APPLICATION NUMBER: 09/23893
PRIOR APPLICATION NUMBER: 09/23893
PRIOR APPLICATION NUMBER: 09/27800
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/27800
PRIOR SERVING DATE: 2001-08-25
PRIOR APPLICATION DATE: 2001-
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo s
US-10-453-372-2
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       GTGGCGCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCCAGATCCTGCGGGTGCGC
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Conservative:
Mismatches:
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Gaps:
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Length: Matches:	, Inc. DSITIONS, KI TIFICATION, CANCER ,284 ,284 71 71 71 74 88		į	CCACGCCCCGTGCCC		TCGGGCCGCGAGAGC	ACCACGCTGCAGGGCCTGGCGGCGG	hheGlyProLeuArgGly	ArgvalserTrpAla	agcctccgcgtgagttgggccccagcgctgggctcagccgc	AlaProGluGluAlaG	–ద	GlyAlaSerGlyPro	; ; ; ; ; ; ; ; ; ; ; ; ;	
3063 128	, AND SESSMENT,		(GCCCCGCGCCCCGACCCC 	AlaLeuSerAla	GCGCTGTCCGCC	gcgccggcaccg	GCGGGGAGGCGCAG lyGlyGluAlaGln	LaProAlaLeuGlyS	CCAGCGCTGGGC	3lyProGluArgI	GGCCAGAGCGC	GluSerGlyAla		
	PREVENTION,			н — О	œ —	O i				— A	gilevalile	TCATC	_' GlyProAla		
	AND			1236 440	20	1176	1116 400	380	60	996	340	936	320	903	300

Db 698 LeuValAsnValThrAlaGluTyrGluAspGlyPheSerIleProLeuAlaGlyGluGlu 717 Oy 757	Deery MacCh: 37.3% Hismaches: 374 Company MacCh: 1754) x US-11-186-284-26 (1-3063) US-10-699-035A-5 (1-1254) x US-11-186-284-26 (1-3063) Dy ACAGGGGACCTCANTTYCCTCTGGTGGACAACTCCTCCACTACGAACTCTCC 153 PA CAGGGTTCGGAATTTTTTOGGGACACTCTCACTACGACCTCCTCACTACGACTCTCC 153 Dy 154 CGGTTCGGAATTTTTTTOGGGACACTCGTGGCCACCACCACCACCACCACCACCACCACCACCACCACC	
US-10-699-035A-5 (1-1254) x US-11-169-041-160 (1-517) Qy 106 ATGTTCCTGCTGGACAGCTCAGCGAGGGTCTCACCTACGAGGTTCCCCGGGTTCGGGAG 165 ::: ::: :::	De 11-12	

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RESULT 4
US-11-182-016-20
US-11-182-016-20
; Sequence 20, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE
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|GluValThrSerTyrGlyPheLysThrAsnTrpSerProAlaGlyGluAsnValPheSer
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          SUBSTRATE
            (TKS)
            PROTEINS
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; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1717
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OTHER INFORMATION:
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|ProArgCysAlaGlyLeuGlyThrAlaGlyHisGlyAlaGlyGlySerSerArgAlaArg
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                                                              LeuCysSerAlaGlyArgSerTrpAlaGlySerGlyGlyCysAlaGlyCysThrGlyPro
                                                                                                                                                                    TrpProProSerGlyProAlaAlaThrAlaLeuLeuProAlaGlyThrMetGlyGlyGly
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR PFLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059913
                                                                                                                                                                                                                           US-10-699-035A-5 (1-1254) x US-10-131-826A-294 (1-915)
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PRIOR APPLICATION NUMBER: 60/059588
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PRIOR FILING DATE: 1997-09-17
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                                                                                    106 ATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGGTTCGGGAG
                                         59 ValPheIleIleAspSerSerArgSerValAsnThrHisAspTyrAlaLysValLysGlu
                                                                                                                                  45 AlaLeuLeuGluSerSerCysGluAsn-----
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Watanabe, Colin K
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Gurney, Austin L.
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Filvaroff, Ellen
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RESULT 6
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Query Match:
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                                                                                                                                       Pred. No.:
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Publication No. US20050260713A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 39
LENGTH: 956
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TITLE OF INVENTION: Polypeptides and Nucleic Acids
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
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SOFTWARE PROPERTY AND THE SOFTWARE PROPERTY 
                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILLING DATE: 2001-07-24
APPLICATION NUMBER: 60/322,358
FILING DATE: 2001-09-14
APPLICATION NUMBER: 60/294,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/315,617
FILING DATE: 2001-08-29
APPLICATION NUMBER: 60/307,506
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FILING DATE: 2000-12-20
APPLICATION NUMBER: 60/311,613
FILING DATE: 2001-08-10
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                                Percent Similarity:
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                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                            SOFTWARE: pt_SEQ_genes Version
SEQ ID NO 1431
LENGTH: 1366
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Publication No. US20050255114A1
GENERAL INFORMATION:
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APPLICANT: Stache-Cra
APPLICANT: Andarmani,
ADDITCANT: Tanc V T
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tang, Y. Tom TITLE OF INVENTION: Methods for Diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                    No.:
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US-10-699-035A-5 (1-1254) x US-11-186-284-31 (1-1366)
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, KITITLE OF INVENTION: METHODS FOR IDENTIFICATION,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMOL-029PZRNM
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                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2005-07-21
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No. US20050266493A1
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84	24 CCTGGCCCTGAGCTTGCGGCTGGCGCTGGCGCGGGAGCGGGAGCGCGGTCCACCAGC 83 :::	-10-699-035A-5 (1-1254) x US-11-186-284-35 (1-1496)	7 Gaps:	PERCENIC SIMILATITY: 33.3% CONSERVACTIVE: 22 Best Local Similarity: 28.4% Mismatches: 164 Onery March: 9.0% Indels: 136	5.: 5./5e-Ub Length: 215.00 Matches: 215.00 Concention.	ment Scores:	OKGANISM: Homo Sapiens -11-186-284-35	1496 RT	FastSEQ for	PRIOR APPLICATION NUMBER: US 60/381,988 PRIOR FILING DATE: 2002-05-20 NUMBER OF SEO ID NOS: 228	APPLICATION NUMBER: US 60/361, FILING DATE: 2002-03-05		PPLICATI	CURRENT APPLICATION NUMBER: US/11/186,284 CURRENT FILING DATE: 2005-07-21	OF INVENTION: METHODS FOR IDENTIFICATION, ASSI OF INVENTION: THERAPY OF COLON CANCER REFERENCE: MPMO1-029PARM	Ĭ	APPLICANT: Schlegel, Kobel APPLICANT: Monahan, Orn E. ADDITCANT. Thibodesu Orn N		ANT: Millennium Pha ANT: Berger, Allis	Sequence 35, Application US/11186284 Publication No. US20050266493A1 GENERAL INFORMATION:	35	588 ArgGlyGluArgGlyProProGlyGlu 596	1209	568 GlyLysProGlyGluArgGlyLeuHisGlyGluPheGlyLeuProGlyProAlaGlyPro 587	1152	551 ProProGlyPheGlnGlyLeuProGlyProSerGlyProAlaGlyGluVal	1000	1035CGGGGAGGCGCAGCGGGTGGAGGTGCCCGCGGGGCCGCAACTGCACCACGCTGCAGGG	516 AlaGl	990

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rgGlyAsp 1069	GlyAsnAspGlyThrProGlyArgAspGlyAlaValGlyGluArgGlyAspArCGCAACTGCACCACGCTGCAGGG	1050 1068 1070	
- 10	GCAGTTCGGGCCGCTGCGGGGCGGGGAGCGCAGCGGGTGGAGGTGCCCGCGGG	2 2	
ACCACGT 1013	CAGCCTCCGCGTGAGTTGGGCCCCAGCGCTGGGCTCAGCCGCGGCGCTCGGCTACCACGT	954 1032	
	 ThrProGlyLysValGlyProThrGlyAlaThrGlyAspLysGlyProProGlyProVal	1012	
	GCGCACGCGGCCAGAGGAGGCCGGGCCAGAGCGCATCGTCATCTCCCACGCCCGGCCGCG	94	
TGCGGGT 893	CGACGTGGCGCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATCCTGCGGGT :::	834 997	
CGGACTA 833	GCAGCTGCCAGGGACCGGACACGGACTGGACCCGGACACGGACACGGACTA	983	
	AspProGlyGluAspGlyGlnProGlyProAspGlyProProGlyPro	967	
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AGCTCCA 653	CATCATTGTCCAAGAGCTGAGGGGCTCCATTCTCGCGATGCGGCCGCAGCAGCAGCTCCA	597 940	
ProGly 939	GlyProLeuGlyGluProGlyLysGluGlyPro	927	
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	cctgggcgtcaccgtgttcattgtcagc	480	
gValGly 915	GlyProProGlyAlaThrGlyPheProGlySerAlaGlyArgValGly	900	
479	CAGCGACCCTGTGGGGCCCCCATGCAGGAGCTCAAGGA	441	
	ArgGlyThrGln	896	
GCGGCTC 440	AGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATG	381	
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	CAGCTCGGGTGAGGCTGCCCAGCGATGCGGTGCGTGCTTCTGCCCAGCGCATGGG	73	`
uProGly 864	<pre>AlaGlyProGlnGlySerAspGlyGlnProGlyValLysGlyGluProGlyGluProGly</pre>	845	
GCCAGCA 272	gcgTgcCagTcTggTgcacgTgggCagTcggcCaTaCaccgagTTccccTTcg	213	
.1GlyPhe 844	GGTGGCTCCACTGGCCCCTGGGCACCGGGGCCCT	180 825	
yProPro 824	LeuGlyGluLysGlyGluProGlyProArgGlyLeuValGl	809	
GGCAGCT 179	CTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAGCT	123	
aGlyLeu 808	${\tt GlyAsnAspGlyAlaGlyGlyLeuProGlyProLeuGlyProProGlyProAlaGlyLeu}$	789	

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APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785C1P4CN
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-09-17
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Query Match:
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SEQ ID NO 243
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                                                                          592 ProGlyLysAlaGlyGluArgGlyValProGlyProProGlyAlaValGlyProAlaGly 611
                                       48 ---GCTGGCGCGGAGCGCGCGGAGCGCGGTCCACC-----AGCATCAGCCCC-----
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Wang, Zhiwei
Wehrman, Tom
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Asundi, Vinod
Chen, Rui-hong
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	.1 CGTGCAGTTCGGGCCGCTGCGGGGGGGGGGGGGAGGCGGGGT 1052	1011
		892
	1 GCGCAGCCTCCGCGTGAGTTGGGCCCCAGCGCTGGGCTCAGCCGCGGCGCCTCGGCTACCA 1010	951
	::: 2 GlyAlaThrGlyPheProGlyAlaAlaGlyArgValGlyProProGlyProSerGlyAsn 891	872
		918
	2 ProlleGlyAsnValGlyAlaProGlyAlaLysGlyAlaArgGlySerAlaGlyProPro	85
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	b TECTTCTECCAEGGATGACACCCACACTGGCCTGGCTGGTCTATGCCAAGGA 365	675
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	ATACACCGAGTTCCCCTTCGGCCAGGAGCTCGGGTGAGGCTGCCCAGGATGCGGTGCC	246
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	6 TCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGTCGGCC 245	186
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	<pre>2 LysAspGlyGluAlaGlyAlaGlnGlyProProGlyProAlaGlyProAlaGlyGluArg 631</pre>	612
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15 GGCGCTCGG	Scores: 8.52e-06 Length 212.00 Matche 212.00 Conser milarity: 33.6% Conser .Similarity: 27.5% Mismat th: 8.9% Gaps:	SULT 11 :11-186-284-28 sequence 28, Application US/11186284 Publication No. US2005266493A1 GENERAL INFORMATION: APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Kamatkar, Shubhangi APPLICANT: Kamatkar, Shubhangi APPLICANT: Monahan, John B. APPLICANT: Monahan, John B. APPLICANT: Thibodeau, Stephen N. APPLICANT: Monahan, John B. APPLICANT: Monahan, John B. APPLICANT: MONABER: USOPERING, KITS, AND TITLE OF INVENTION: MOTEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: MOTEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, MONEST. USOPERING TITLE OF INVENTION: MOTEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, APPLICATION NUMBER: US/11/186,284 CURRENT APPLICATION NUMBER: US/10/301,822 PRIOR APPLICATION NUMBER: US/0/301,822 PRIOR APPLICATION NUMBER: US 60/339,971 PRIOR APPLICATION NUMBER: US 60/339,971 PRIOR APPLICATION NUMBER: US 60/361,978 PRIOR FILING DATE: 2002-03-05 PRIOR APPLICATION NUMBER: US 60/361,978 PRIOR APPLICATION NUMBER: US 60/361,978 PRIOR FILING DATE: 2002-05-20 NUMBER OF SEQ ID NOS: 28 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 28 LENGTH: 1464 TYPE: PRT THE OF THE OF THE ORDER OF T	999 roMetGlyProProGlyLeuAla 1006	1227 CCCGGGGACCGCCAGCCGTGAGC 1249	985 GlnGlyProSerGlyAlaSerGlyGluArgGlyProProGlyP 999		966 GlnArgGlyGluArgGlyPheProGlyLeuProGlyProSerGlyGluProGlyLys 984	1119 GACCGTGACCGCCGCCTTCCGCTCGGGCCGCGAGAGCGCGCCTCTCCGC 116	 	CCTGGCCCTGGCACCGC	 930 ProAlaGlyGluLysGlySerProGlyAlaAspGlyProAlaGlyAla 945	1053GGAGGTGCCCGCGGGCCGCAACTGCACCACGCTGCAGGG 109

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	GlyAlaThrGlyPheProG
	891
	843 GCTAGTGCCTGAGTCCAACGTGCGCCCCCGAGGCCCCAGATCCTGCG
	GACTGATCTGGGCCGGCTCGACCCGGACACGGACTACGACGTGGC
<u>-</u>	735 GCTGGTGCCCAGCGCCCAGCCGGGGGCTGCCAAGACGCCAGCAGCAGCGAACGCCAC 794 798 AlaProGlyAspArgGlyGluProGlyProProGlyProAlaGlyPheAlaGlyProPro 817
	675 CGGCTTCCGCCTGGCCACCCCTGCTGACCGCAGACTCGGGCTACTATGTGCTGGA 734
	642GLAGCAGCTCCATGCCACGAGATCACGTCCAG 674
	594 GCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTCGCGATGCGGCC 641
	534 GTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCT 593 ::: 742Ly8GlyAspArg 745
· 	477 GGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCT 533
	420 GTGGGTGACAGATGGCGGCCTCCAGCGACCCTGTGGGCCCCCATGCAGGAGCTCAA 476
	366 ACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGT 419
	306 TGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGCGCTGGTCTATGCCAAGGA 365
	246 ATACACCGAGTTCCCCTTCGGCCAGCACCAGCTCGGGTGAGGCTGCCCAGGATGCGGTGCG 305 :::
	186 TCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGTCGGCC 245 643 GlnGlyLeuProGlyProAlaGlyProProGlyGluAlaGlyLy8ProGlyGluGlnGly 662
	126 AGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAGCTGGTGGC 185
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SEQ ID NO 2
LENGTH: 1464
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TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
FILE REFERENCE: 06275-254US1
CURRENT APPLICATION NUMBER: US/11/021,603
CURRENT FILING DATE: 2004-12-21
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PRIOR FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/GB00/04741
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: GB 9929487.8
PRIOR FILING DATE: 1999-12-15
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126 AGCCAGCGTCTCTCACTACGAGTTCTCCCGGGGTTCGGGAGTTTGTGGGGGCAGCTGGTGGC 185
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OY 246 ATACACCGAGTTCCCCTTCGGCCAGCACAGCTCGGGTGAGGCTGCCCAGGATGCGGTGCG 305	Oy 186 TCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGTCGGCC 245	Oy 126 AGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTCTGGGGCAGCTGGTGGC 185 ::::::	Qy 93	Qy 48GCTGGCGCGGAGCGCGGGGCGCGGAGCGCCC 92	Qy 15 GGCGCTCGGCCTGGCCCTGAGCTTGCGGCTGGC 47 Db 575 GlyAlaArgGlyGlnAlaGlyValMetGlyPheProGlyProLysGlyAlaAlaGlyGlu 594	035A-5 (1-1254) x US-10-821-234-1096 (1-1467	212.00 Matches: 140 it Similarity: 33.6% Conservative: 31 ocal Similarity: 27.5% Mismatches: 168 Mismatches: 170	-821-234-1096 ment Scores: NO . 8 528-06	O 1096	PPLICATION NUME ILING DATE: 200 DF SEQ ID NOS: E: pt SEQ genes	; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia; FILE REFERENCE: 821A; CURRENT APPLICATION NUMBER: US/10/821,234; CURRENT FILING DATE: 2004-04-07	ANT: Labat, Ivan ANT: Stache-Crain, Birgit ANT: Andarmani, Susan ANT: Tang, Y. Tom	US-10-821-234-1096 US-10-821-234-1096, Application US/10821234 ; Sequence 1096, Application US/10821234 ; Publication No. US20050255114A1 ; GENERAL INFORMATION:	Db 999 roMetGlyProProGlyLeuAla 1006	985 GlnGlyProSerGlyAlaSerGlyGluArgGlyProProGlyP	1167 GluargelyGluargGlyPheProGlyLeuProGlyProSerGlyGluProGlyLys 1167 GluargGlyGluArgGlyPheProGlyLeuProGlyProSerGlyGluProGlyLys	 946 ProGlyThrProGlyProGlnGlyIleAlaGlyGlnArgGlyValValGlyLeuProGly	Db 930 ProAlaGlyGluLysGlySerProGlyAlaAspGlyProAlaGlyAla 945 Qy 1092 CCTGGCGCCGGGCACCGCCTACCTGGT 1118

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	GAGCAGCTCCATGCCACGGAGATCACGTCCAG 674	642 769
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PRIOR APPLICATION NUMBER: 09/93,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/93,404
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PRIOR APPLICATION NUMBER: 09/63,451
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                                             1153 TCTCGCGGCCCGAGCGGAAGGCGGCGGTCA------CGGTCACCAGGTAGGCGG 1106
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
FITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AN
FITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESS
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION UNMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
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US-11-186-284-28
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SOFTWARE: FastSEQ for W
SEQ ID NO 28
LENGTH: 1464
TYPE: PRT
                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                              US-10-699-035A-5 (1-1254) x US-11-186-284-28 (1-1464)
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
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-Q=/Abss/ABSSWEB spool/US10699035/runat 13022006 062444 25463/app_query.fasta_1
-Q=/Abss/ABSSWEB spool/US10699035/runat 13022006 062444 25463/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINANTCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US10699035 @CGN 1 17 @runat 13022006 062444 25463 -NCPU=6 -ICPU=3
-NORMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPDXT=0.5 -FGAPOP=6 -FGAPEXT=7
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A;Gene: Col14A1

G;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimG;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimF;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3B>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3B>
F;441-823/Domain: fibronectin type III repeat homology <FN3B>
F;623-707/Domain: fibronectin type III repeat homology <FN3B>
F;741-823/Domain: fibronectin type III repeat homology <FN3B> A;Molecule type: mRNA
A;Residues: 1-1857 <MAE>
A;Residues: 1-1857 <MAE>
A;Cross-references: UNIPARC:UPI000017123C; EMBL:X70792; NID:g288874; PIDN:CAA50063.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics: Eur. J. Biochem. 212, 483-490, 1993 A;Title: Complete primary structure of chicken collagen XIV. A;Reference number: S31211; MUID:93185668; PMID:8444186 collagen alpha 1(XIV) chain precursor, short form - chicken C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003 C;Accession: S31212 R;Waelchli, C:; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Bur. J. Biochem. 212, 483-490, 1993 Eur. J. Biochem. 212, 483-490, 1993 RESULT S31212 Pred. A; Reference number: A; Accession: S31212 Percent Similarity: Best Local Similari F;922-1009/Domain: fibronectin A;Status: nucleic acid sequence not Query Match: F;1040-1205/Domain: No.: Similarity: von 1.15e-13 268.00 50.5% 33.0% Willebrand factor shown; translation not shown III repeat homology <FN3H> actor type A repeat homology <VWA2> Length:
Matches:
Conservative:
Mismatches:

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A;Gene: Coll4Al
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycopr
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWAl>
                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1888 <TTU>
A;Residues: 1-1888 <TTU>
A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:g288872;
A;Cross-references: UNIPROT:P32018; Winterhalter, K.H.; Trueb, B.
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
578476
collagen alpha 1(XIV) chain precursor,
collagen ellus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence revision
C;Accession: S78476; S31211
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A; Residues: 1-416;1460-1811,1843-1888 <WAE>
A; Cross-references: UNIPARC: UPI00001773F4; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: S78476
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AlaAspPheAsnPheMetAsnSerIleValGluGlyLeuThrArgThrValCysSerArg
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ProAlaLysAsnLeuArgAspAlaGlyIleGluLeuPheAlaIleGlyValLysAsnAla
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C;Species: Gallus gallus (chicken)
C;Accession: A40020; A34485; B34485; A28037; S23814; S22754; S28811
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C;Accession: A40020; A34485; B34485; A28037; S23814; S22754; S28811
C;Accession: A40020; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Oba
J, Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site
A;Accession: A40020
A;Molecule type: mRNA
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homology
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AspIleValIleLeuValAspGlySerTrpSerIleGlyArgPheAsnPheArgLeuVal
                                                                                                       ||| ::: ::::: |||||:::
AlaAspPheAsnPheMetAsnSerIleValGluGlyLeuThrArgThrValCysSerArg
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F;630-711/Domain: fibronectin type III repeat homology <FN3C>
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F;905-986/Domain: fibronectin type III repeat homology <FN3F>
F;995-1076/Domain: fibronectin type III repeat homology <FN3H>
F;1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F;1197-1361/Domain: von Willebrand factor type A repeat homology <FN3H>
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F;1384-1465/Domain: fibronectin type III repeat homology <FN3J>
F;1474-1557/Domain: fibronectin type III repeat homology <FN3J>
F;1566-1647/Domain: fibronectin type III repeat homology <FN3J>
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A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of A;Reference number: $23814; MUID:92362621; PMID:1323460
A;Reference number: $23814 MUID:92362621; PMID:1323460
A;Residues: 'X',1331,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 A;Reference number: S22254; MUID:88087065; PMID:3121603
A;Reference number: S22254; MUID:88087065; PMID:3121603
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A;Residues: 2831-2832,'T',2834,'X',2836-2843;3002-3014 CDUB>
A;Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45
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J. Biol. Chem. 264, 19772-19778, 1989
A;Title: Type XII collagen. A large multidomain molecule with partial homology to ty A;Reference number: A34485; MUID:90062079; PMID:2584192
A;Accession: A34485
A;Molecule type: mRNA
A;Residues: 2456-2758; A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A;Cross-references: UNIPARC:UPI0000171233; EMBL:U05137; NID:9211284; PIDN:AAA48635.1
A;Accession: B34485
A;Molecule type: protein
A;Residues: 2772-2792;2846-2873 <GOR2>
A;Residues: 2772-2792;2846-2873 <GOR2>
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A;Cross-re
A;Note: in
R;Gordon,
J. Biol. C
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A;Rosidues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280
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A;Title: The two splice variants of collagen XII share
A;Reference number: S28811; MUID:93042014; PMID:1420368
A;Accession: $28811
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A;Cross-references: UNIPARC:UPI00001712F4; EMBL:M17375; NID:g211649;
A;Note: this sequence has been revised in reference A34485
R;Koch; M.; Bernasconi, C.; Chiquet, M.
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R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by A;Reference number: A28037; MUID:87317590; PMID:3476925
A;Accession: A28037
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;332-414/Domain: fibronectin type III repeat homology <FN3B>
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Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
Cross-references: UNIPARC:UPI0000171233; EMBL:J05137; NID:g211284; PIDN:AAA48635.1;
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von Willebrand factor type A repeat homology
IIID #status predicted <IIID>
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F;1655-1738/Domain:
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F;1847-1928/Domain:
F;1847-2019/Domain:
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Query Match:
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Cascagnola, P.; Gennari, M.; Dublet, B.; Canc. J. Biol. Chem. 268, 12177-12184, 1993
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F;2509-2750/Domain:
F;2751-2902/Domain:
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fibronectin type III repeat homology <FN3N>
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von Willebrand factor type A repeat homology
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F;40-204/Domain: von Willebrand factor type A repeat homology <VW
F;236-317/Domain: fibronectin type III repeat homology <FN3A>
F;326-409/Domain: fibronectin type III repeat homology <FN3A>
F;418-498/Domain: fibronectin type III repeat homology <FN3C>
F;507-591/Domain: fibronectin type III repeat homology <FN3D>
F;625-707/Domain: fibronectin type III repeat homology <FN3D>
F;716-798/Domain: fibronectin type III repeat homology <FN3E>
F;716-798/Domain: fibronectin type III repeat homology <FN3G>
F;806-893/Domain: fibronectin type III repeat homology <FN3G>
F;924-1089/Domain: von Willebrand factor type A repeat homology <FN3G-
F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F;1511-553/Domain: triple helical domain COL1 #status predicted
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Bur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member
A;Reference number: S17035; MUID:92037585; F
A;Accession: S17035
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A;Title: Type XIV collagen is a variant of
A;Reference number: S22916; MUID:92339443;
A;Accession: S22916
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A;Residues: 1472-1660 APT>
A;Cross-references: UNIPARC:UPI00000006A2; EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PII
R;Trueb, J; Trueb, B
Eur. J. Biochem. 207, 549-557, 1992
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A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide translation
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Pred. No.:
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A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A;Cross-references: UNIPARC:UPI0000173C49
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A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439
A;Cross-references: UNIPARC:UP10000173C48
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A; Residues: 1-1747 <GER>
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A;Residues: 1472-1659 <GORl>
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  AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCG
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                                                                                                                                                                      GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
                                          ArgLeuPheLeuGluAsnLeuValSerArgPheAsnValGlySerGluLysThrArgVal 81
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Conservative:
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PMID:1339349
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A;Residues: 78-493 <ARG>
A;Residues: 78-493 <ARG>
A;Residues: 78-493 <ARG>
A;Cross-references: UNIPARC:UPI000004F1EE; GB:M14792; NID:g211545; PIDN:AAA48695.1;
A;Cross-references: UNIPARC:UPI000004F1EE; GB:M14792; VID:g211545; PIDN:AAA48695.1;
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat homology <VWA1>
F;37-204/Domain: von Willebrand factor type A repeat homology <VWA2>
F;270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argr J. Biol. Chem. 264, 8126-8134, 1989
A;Title: Structure of the gene for cartilage matrix protein, a modular protein of the exgrins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor. A;Reference number: A33809; MUID:89255246; PMID:2542265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cartilage matrix protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33809; A25364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goeti Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987. A;Title: Structural features of cartilage matrix protein A;Reference number: A26364; MUID:87092429; PMID:3025875 A;Accession: A26364.
                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P05099; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; GB:X123
R;Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-493 < KIS>
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                                                                                                                  US-10-699-035A-1 (1-537) x A33809
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|||:::::|||:::||| ||| ValGluGluGluGluLysGluIleLysGlyThrIleAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein A;Reference number: $66522; MUID:96270751; PMID:8665920 A;Accession: $66522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cartilage matrix protein precursor - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S66522
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A;Gene: CMP
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A; Residues: 1-500 < ASZ >
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                                                                                                                                                                                                                                                                                                F;277-441/Domain:
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                                                                                                                                                                                                                                                                                                                  231-266/Domain:
                                                                                                                                                                                                 Local Similarity:
                                                                                                                                                                                                                                                 No:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.; Hauser, N.; Studer, D.; Paulsson,
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65
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                                                                                  GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
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                                CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCC 123
                                                             AspLeuValPheValValAspSerSerArgSerValArgProValGluPheGluLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrAlaAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTGGCGCTGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACT
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                                                                                                                                                                                                                                                                                              'von Willebrand factor type A repeat homology <VWA2:
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239.50
52.4%
34.8%
22.8%
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                               Gaps:
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                                                                                                                                                                 500
57
29
75
3
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A; Molecule type: mRNA
A; Residues: 157-290, 'L', 292-496 <JE2>
A; Cross-references: UNIPARC:UPI000016A6E8;
C; Genetics:
                                                                                                                                                                                                                                                                                                                                        C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand C;Keywords: glycoprotein; homotrimer F;1-22/Domain: signal sequence #status predicted <SIG>F;23-496/Product: cartilage matrix protein #status predicted <MAT>F;39-206/Domain: von Willebrand factor type A repeat homology <VWA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage matrix protein precursor - human
c;Species: Homo sapiens (man)
C;Date: 12-Jul-1991 #sequence revision 12-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37979; B37979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; J. Biol. Chem. 265, 19624-19631, 1990
J. Biol. Chem. 265, 19624-19631, 1990
A;Tille: Structure and chromosomal location of the human gene encoding cartilage matri
A;Reference number: A37979; MUID:91060568; PMID:2246248
                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                            F;227-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;76.344/Binding site: carobhydrate (Asn) (covalent) #status predicte
F;721-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1 C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1p35-1p35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:127280; OMIM:115437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: CRTM
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A; Residues: 1-496 <JEN>
A; Cross-references: UNIPROT: P21941; UNIPARC: UPI000004F1ED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A37979
US-10-699-035A-1 (1-537) x A37979
                                                                      Query Match:
                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                         No.:
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                                                 7.02e-11
233.50
50.3%
35.0%
22.3%
(1-496)
                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                              Indels:
Gaps:
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                                              496
62
27
87
1
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C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #text_change C;Date: 04-Nov-1994 #text_change C;Date: 04-Nov-1994 #text_change C;Accession: A54849; PH0844; S16316; I56328; A30226; I94686
C;Accession: A54849; PH0844; S16316; I56328; A30226; I94686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary set A;Reference number: A54849; MUID:94327588; PMID:8051117
A;Accession: A54849
                                                                                                                                                                                   A;Molecule type: manA
A;Residues: 'EER', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528, 'C'
A;Cross-references: UNIPARC:UPI000017A139, DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:)
A;Experimental source: keratinocyte
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mal
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VI collagen: cDNA cloning and chromosomal mapping of the gene.
A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A;Title: Molecular cloning and characterization of type A;Reference number: PH0844; MUID:92231902; PMID:1567409
A;Experimental source: keratinocyte R;Gammon, W.R.; Abernethy, M.L.; Pac J. Invest. Dermatol. 99, 691-696, 19
                                                                                       A; Residues: 815-892, 'E', 894-1439 < PAR>A; Cross-references: UNIPARC: UPI000016A722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-2944 <CHR>
A;Cross-references: UNIPROT:Q02388; UNIPARC:UPI000017A138; GB:L02870; NID:g987124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen alpha 1(VII) chain precursor -
                                                                                                                                                        Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Accession: PH0844
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                                M.L.; Padilla,
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                                                                                           GB:M65158; GB:S49017; NID:g180914; PIDN:AAA9
                                   Prisayanh, P.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-Jul-2004
                                Cook, M.E.; Wright,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
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A;Molecule type: mRNA
A;Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Cross-references: UNIPARC:UPI000016B3AC; GB::S51236; NID::g262308;
A;Cross-references: UNIPARC:UPI000016B3AC; GB::S1236; N.P.; Glanville,
R;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville,
J. Biol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase
A;Reference number: A30296; MUID:89139437; PMID:2537292
A;A;Accession: A30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and A;Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Comment: Prolines and lysines at the third position ed and subsequently O-glycosylated.
C;Genetics:
                                                                                                                                                                                                                                                                                                       F;954-1045/Domain: fibronectin type III repeat hom F;1052-1219/Domain: von Willebrand factor type A r F;1170-1172/Region: cell attachment (R-G-D) motif F;1189-1253/Region: cysteine/proline-rich F;1254-2783/Region: interrupted helical F;1254-2783/Region: cell attachment (R-G-D) motif F;2553-2555/Region: cell attachment (R-G-D) motif F;2553-2555/
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A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'I
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A:None: two reported peptides cannot be reliably located
                                         F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;337,786,1109/Binding site: carbohydrate (Asn) (covalent) #status predictor
F;2167,2176,2185,2188,2644,2667,2673/Modified site: 4-hydroxyproline (Pro)
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: structural component of extracellular polymer associated C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxyly; F;1-16/Domain: signal sequence #status predicted <SIG> F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
    F;2634,2802,2804/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:COL7A1; EBR1; EBD1; A;Cross-references: GDB:128750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3349-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification
A;Reference number: A55255; MUID:94224777; PMID:8170945
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A;Residues: 2395-2871,'S',2873-2944 <RE2>
A;Cross-references: UNIPARC:UPI000016A724;
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, R.W.; Burgeson,
                                                                                                                                                                               predicted
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Alignment Scores:

No.:

1.92e-10 227.50

Length: Matches:

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collagen alpha 3(VI) chain precursor - chicken (C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Accession: A37797; A34270; A32674 C;Accession: A37797; A34270; A32674 R;Dollana, R.; Bonaldo, P.; Colombatti, A. J. Ccll Biol. 111, 2197-2205, 1990 A;Title: Multiple forms of chicken alpha3(VI) collagen chain generated by a;A;Reference number: A37797; MUID:91035630; PMID:1977751 A;Accession: A37797
             A;Molecule type: mRNA
A;Residues: 224-2871 &BON>
A;Residues: 224-2871 &BON>
A;Coss-references: UNIPARC:UPI0000173C38; GB:M24282
A;Note: the authors translated the codon TTC for residue 19
R;Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 264, 20235-20239, 1989
A;Title: The carboxyl terminus of the chicken alpha3 chain
A;Reference number: A32674; MUID:90062147; PMID:2584214
A;Accession: A32674
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A37797
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A;Title: Structural and functional features of the alpha3 chain in A;Reference number: A34270; MUID:90212613; PMID:2322559
                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A;Cross-references: UNIPROT:P15989; UNIPARC:UP10000173C31; UNIPARC:UP10000173C32;
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F;840-1004/Domain: von Willebrand factor type A repeat homology < VW05>
F;840-1004/Domain: von Willebrand factor type A repeat homology < VW05>
F;1033-1197/Domain: von Willebrand factor type A repeat homology < VW06>
F;1237-1400/Domain: von Willebrand factor type A repeat homology < VW07>
F;1439-1604/Domain: von Willebrand factor type A repeat homology < VW08>
F;1639-1804/Domain: von Willebrand factor type A repeat homology < VW08>
F;1639-12010/Domain: von Willebrand factor type A repeat homology < VW08>
F;1634-2798/Domain: von Willebrand factor type A repeat homology < VW09>
F;1043-2798/Domain: collagenous #status predicted <COL>
F;2047/Region: cell attachment (R-G-D) motif
F;2153-2153/Region: cell attachment (R-G-D) motif
F;2159-2161/Region: cell attachment (R-G-D) motif
F;2159-2161/Region: cell attachment (R-G-D) motif
F;2153-2159/Domain: non-collagenous #status predicted <CNC>
F;2045-2577/Domain: von Willebrand factor type A repeat homology < VW11>
F;2653-2806/Domain: von Willebrand factor type A repeat homology < VW12>
F;203-2806/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
F;2015-2016/Region: animal Kunitz-type proteinase inhibitor homology < CON
F;201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (Asn) (cov
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A;Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI0000173C3A; GB:M24282 C;Genetics:
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US-10-699-035A-1 (1-537) x A37797 1.45e-09 216.50 48.0% 33.5% 20.6% (1-3137)Length:
Matches:
Conservative: Gaps: Mismatches: Indels:

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178 AspAlaValGluGlyGluLeuLysGluTleAlaSerArgFroPheAspThrHisLeuPhe 197	418 CGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTG 474	158 AlaLeuProSerSerValLeuLysSerAlaHisValAsnMetIleAlaValGlyValGln 177	358 GGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTTTCATTGTCAGCACCGGC 417	138 SerGluGlyValProGlnValIleIleValLeuThrAspGlyGlnSerGlnAspAspVal 157	301CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCCTGTG 357	118 GlyLysGlyLeuGluTyrLeuIleGluAsnHisLeuThrLysAlaAlaGlySerArgAla 137	CATCAGG	98 AsnGlnAspValLeuSerHisIleAlaAsnMetProTyrMetGlyGlyGlySerLysThr 117	184 GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACT 243	78 AlaLeuValGlnPheSerGlyAsnProHisThrGluPheGlnLeuAsnThrTyrProSer 97	124 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGACACAGCTCG 183	58 ArgGluPheLeuTyrAspValValLysAlaLeuAspValGlyGlyAsnAspPheArgPhe 77	64 CGGGAGTTTGTGGGGCACTGGTGGCTCCACTGCCTGGGCACCGGGGCCCCTGCGTGCC 123	38 AspīleIlePheLeuValAspSerSerTrpSerTleGlyLysGluHisPheGlnLeuVal 57	4 GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCCGGGTT 63	

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A;MOJecule type: mRNA
A;Residues: 1-741 <AAA>
A;Cross-references: UNIPROT:QBNDE6; UNIPARC:UPI000016ACCB; EMBL:AL137638
A;Experimental source: adult testis; clone DKFZP434J065
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C;Date: 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46488
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
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A;Accession: T46488
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                                                                CCTGTGGGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGC
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|AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGluAsnPheGluValVal
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A; Molecule type: protein
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A; Residues: 574-585;965-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',1508
A; Residues: 574-585;965-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',
A; Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
C1C; UNIPARC:UPI0000173C1D; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
C1C; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C17; UNIPARC:UPI0000173C17;
C1C; UNIPARC:UPI0000173C18; UNIPARC:UPI0000173C17;
C1C; UNIPARC:UPI0000173C18; UNIPARC:UPI0000173C18;
C1C; UNIPARC:UPI0000173C18; UNIPARC:UPI0000173C18
A; Zamussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.

J. Biol. Chem. 267, 24082-24089, 1992
A; Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain
A; Reference number: S28776; MUID:93054780; PMID:1339440
A; Residues: 310-28 < ZAN>
A; Cross-references: UNIPARC:UPI0000173C28
                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 2038-2373 CCH4>
A;Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
A;Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
A;Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
A;Cossidues: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
A;Weil, D.; Mattei, M.G.; Passage, E.; Van Cong, N.; Pribula-Conway, D. Am. J. Hum. Genet. 42, 435-445, 1988
A;Title: Cloning and chromosomal localization of human genes encoding A;Reference number: A29848; MUID:88161046; PMID:3348212
A;Accession: C29848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 32-126, AK', 129-136, 'L', 138-236 <ZA2>
A;Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1; A;Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1; A;Choss-reference, K.; Deutzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, M. Eur. J. Biochem. 168, 309-317, 1987
A;Title: Characterization of three constituent chains of collagen type VI by peptide A;Reference number: S00126; MUID:88029444; PMID:3665927
A;Accession: S00245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: the mRNA portion of the sequence corresponds to residues 2092-2157 R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Timpl, R. J. Biol. Chem. 263, 18601-18606. The sequence of the triple-helical domain of human collagen type VI. A;Reference number: A31952; MUID:89066644; PMID:3198591 A;Accession: C31952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA; protein
A;Residues: 2024-2046;2092-2156',R';2203-2208,'X',2210-2211,'X',2213-2227;2228-2251;2314
A;Cross-references: UNIPARC:UPI000016A705; UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A;
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A;Residues: 1-30,237-313,'CWW',318-322,'AR',326-1815,'FD',1818-1819,'ID',1822-3176
A;Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:g3127925
A;Accession: S24465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P12111; UNIPARC:UPI0000126D4F; R;Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.;
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A;Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:g291919; A;Note: part of this sequence was determined by protein sequencing R;Jander, R.; Rautenberg, J.; Glanville, R.W.
Eur. J. Biochem. 133, 39-46, 1983
                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 2092-2151 <WEI>
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N;Contains: collagen alpha 3(VI) chain, splice fort
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FileScal7/Bomain: sequence #status predicted cAMH31>
FileScal7/Bomain: anino-terminal nonhelical #status predicted cAMH31>
FileScal7/Bomain: von Willebrand factor type A repeat homology <WW03>
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A;Note: this sequence cannot be reliably placed and probably represents the results f
R;Mayer, U; Poeschl, E.; Nischt, R.; Specks, U.; Pan, T.C.; Chu, M.L.; Timpl, R.
Eur. J. Biochem. 225, 573-580, 1994
B;Title: Recombinant expression and properties of the Kunitz-type protease-inhibitor
A;Reference number: S48709; MUID:95045506; PMID:7525281
A;Accession: S48709
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C;Keywords: alternative splicing; blocked amino end; cell binding; coiled coil; ext.
E;1.25/Domain: signal sequence #status predicted <SIG>
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C;Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHULA) sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
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A;Note: engineered sequence to allow isolation of the Kunitz-type proteinase inhibitor R;Arnoux, B.; Merigeau, K.; Saludjian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O. submitted to the Brookhaven Protein Data Bank, August 1994
A;Reference number: A52812; PDB:IKNT
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A; Residues: 'MRAWIFFLLCLAGRALAA', 3102-3176 <MAY>
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                                                               Percent Similarity:
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                                   Local Similarity:
7.55e-09
207.50
47.4%
31.4%
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Matches:
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R;Kern, A.; Briesewitz, R.; Bank, I.; Marcantonio, E.E. J. Biol. Chem. 269, 22811-22816, 1994
A;Title: The role of the I domain in ligand binding of the A;Reference number: A55348, MUID:94357930; PMID:7521332
A;Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        integrin alpha-1 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Feb-1995 #sequence_revisio:
C;Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-272 <KER>
A;Cross-references: UNIPROT:O42094; UNIPARC:UPI000017A14E; GB:U10114
F;55-230/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                                GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCCGGGTT
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Best Local Si
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A;Title: Monoclonal antibody MT2 identifies the urodele alpha A;Reference number: 151027; MUID:95246925; PMID:7729585
A;Accession: I51027
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A; Residues: 1-929 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Briesewitz, R.; Epstein, M.R.; Marcantonio, E.E. J. Biol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated forms of the A;Reference number: A45226; MUID:93155124; PMID:8428973
A;Accession: A45226
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C;Species: Homo sapiens (man)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A45226
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                           ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
                                                                                                                                                  GlyIleValGlnTyrGlyGluAsnValThrHisGluPheAsnLeuAsnLysTyrSerSer
                                                                                                                                                                                                                           ThrAlaPheLeuAsnAspLeuLeuLysArgMetAspIleGlyProLysGlnThrGlnVal 181
                                                                                                                                                                                                                                                                                                                                          GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
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GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAAGCGCATGGGT---GACACCCAC
                                                                                                                                                                                        AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG
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F;165-246/Domain: fibronectin type III repeat homology <FN3A>
F;255-33B/Domain: fibronectin type III repeat homology <FN3B>
F;347-427/Domain: fibronectin type III repeat homology <FN3C>
F;347-627/Domain: fibronectin type III repeat homology <FN3D>
F;436-520/Domain: fibronectin type III repeat homology <FN3F>
F;547-632/Domain: fibronectin type III repeat homology <FN3F>
F;641-723/Domain: fibronectin type III repeat homology <FN3F>
F;731-818/Domain: fibronectin type III repeat homology <FN3F>
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular A;Reference number: A40970; MUID:91373351; PMID:1716629
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A; Residues: 1-843 < JUS>
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LysProGluAlaGlySerArgThrGlyValSerLysIleGlyIleLeuIleThrAspGly
                                                                                                             GCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGC
                                                                                                                                                  TyrLysGlyGlyAsnThrLeuThrGlyLeuAlaLeuAsnTyrIlePheGluAsnSerPhe
                                                                                                                                                                                                                              TrpHisLeuAsnAlaPheSerThrLysAspGluValIleGluAlaValArgAsnLeuPro 42
                                                                                                                                                                                                                                                                 ValGlySerGluLysThrArgIleGlyLeuAlaGlnTyrSerGlyAspProArgIleGlu
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                                                                                  GCCGAGAAGCACCTGCACTTTGTG---GACGTGGATGACCTGCACATCATTGTCCAAGAG 516
                            CTG 519
                                                                                                                   PheAlaIleGlyValLysAsnAlaAspValAsnGluLeuGlnGluIleAlaSerGluPro
                                                                                                                                               TTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCT
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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006 062441 25416/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006 062441 25416/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINNATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=Ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10699035 @CGN 1 1 580 @runat 13022006 062441 25416 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -NO POST -NO P
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EMBL; BC059409; AAH59409.1; -; Genomic DNA.
EMBL; AL391244; CA122657.1; -; Genomic DNA.
Ensembl; ENSG00000179403; Homo sapiens.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PP00041; fn3; 2.
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PS50234; VWFA; 1.
                                                                                          GTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTC
                                                                                                              CCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA
                                                                                                                                                                                                                                ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
                                                                                                                                                                                                                                                                        SerGlyGluAlaAlaGlnAspAlaValArgAlaSerAlaGlnArgMetGlyAspThrHis
                                                                                                                                                                                                                                                                                    TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGGATGGGTGACACCCAC
                                                                                                                                                                                                                                                                                                               AlaSerLeuValHisValGlySerArgProTyrThrGluPheProPheGlyGlnHisSer
                                                                                                                                                                                                                                                                                                                            GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGC
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                                                                                                                                  GGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTT
                                                                                                                                                    ProProMetGlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGlyArg
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  (TrEMBLrel.
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RC Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D. Collins F.S. Wagner L. Shemmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullahy S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullahy S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullahy S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RI Droc Narl Dand Schi II c. Dones S.J.M., Marra M.A.,

RI Droc Narl Dand Schi II c. Dones S.J.M.
     RC STRAIN-C57BL/66; TISSUE-Ovary and uterus;

RX MEDLINE=21085660; pubMed=11217851; DOI=10.1038/35055500;

RX MEDLINE=21085660; pubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Kawai J., Shinagawa A., Shibata Y., Konno H., Adachi J., Fukuda S.,

RA Arzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Garriboldi M.,

RA Schriml L.M., Staubli F., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garriboldi M.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Haysehizki V., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99279253; PubMed=10349636; DOI=10.10
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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Hayashizaki
"Functional
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  of.
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  full-length
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     mouse
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     CDNA
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  collection.
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Alignment :
Pred. No.:
                                                                                                       STRAIN-C57BL/6J; TISSUE-Ovary and uterus;
A Adachi J., Aizawa K., Akimura T., Braa A., Hashizume W.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Makamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Nishi K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
A Togawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.

P NUCLEOTIDE SEQUENCE.

C STRAIN-C578L/6J; TISSUE-Ovary and uterus;

C STRAIN-C578L/6J; TISSUE-Ovary and uterus;

X MEDLINE-20530913, Pubmed=11076861; DOI=10.1101/gr.152600;

X MEDLINE-20530913, Pubmed=11076861; DOI=10.1101/gr.152600;

X MEDLINE-20530913, Pubmed=110.70148 N., Sasski N., Carninci P.,

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasski N., Itoh M.,

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

A Yoneda Y., Ishikwa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yoneda Y., Ishikwa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                          Ensembl; ENSMUSGO000042116; Mus m
MGI; MGI:2179729; Vwal.
GO; GO:0005615; C:extracellular sp
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.

STRAIN-FVB/N; TISSUB-COlon;

STRAIN-FVB/N; TISSUB-COlon;

Director MGC Project;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ

EMBL; BC026919; AAH26919.1; -; mRNA.

EMBL; BC036166; AAH36166.1; -; mRNA.

EMBL; BC036166; AAH36166.1; -; mRNA.

HSSP; P18614; IMHP.
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MEDLINE-20499374; PubMed=11042159; DOI-=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Ovary
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                                                     Scores:
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                                                                                                  PS50853; FN3; 2.
PS50234; VWFA; 1.
415 AA; 44709 MW;
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US-10-699-035A-1 (1-537)
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                                                                                       of extracellular matrix proteins.";
FEBS Lett. 517:61-66 (2002).
EMBL; AY030094; AAX38350.1; -; mRNA
HSSP; P18614; 1MHP.
Ensembl; ENSMUSG00000042116; Mus mus
                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequention updat
Von Willebrand factor A-related protein.
Name=Vwa1; Synonyms=4932416A11Rik, Warp;
Mus musculus (Mouse)
                                                 Ensembl; ENSMUSG00000042116; Mus
MGI; MGI:2179729; 4932416AllRik.
MGI: MGI:2179729; Vwal.
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognal Muroidea; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q923K3 MOUSE PRELIMINARY;
   InterPro;
InterPro;
                                                                                                                                                                               MEDLINE=22057805; PubMed=12062410; DOI=10.1016/S0014-5793(02)02579-6; Fitzgerald J., Ting S.T., Bateman J.F.; "WARP a new member of the von Willebrand factor A-domain superfamily
                                      GO:0005615;
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IPR003961; FN III. IPR002035; VWF_A.
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                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4932416All product:VON WILLEBRAND FACTOR A-RELATED
PROTEIN homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ent Similarity:
Local Similarity:
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                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Euarchontoglires; Glires;
Muroidea; Muridae; Murinae; Mus.
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PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44737 MW;
                                                                                                                                                                                  Name=Vwa1; Synonyms=4932416A11Rik;
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Q8C0Q7;
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                          NUCLEOTIDE SEQUENCE
                                                                  [_TaxID=10090;
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SM00060; FN3; 2.
SM00327; VWA; 1.
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RC STRAIN=C37BL/63; TISSUE=Testis;

RX MEDLINB=21085669; PubMcd=11217851; DOI=10.1038/35055500;

RA MADLINB=21085669; PubMcd=11217851; DOI=10.1038/35055500;

RA ALRAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kabai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Kakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Bolfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Hordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Myrshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashtzaki Y.;
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Carninci P., Hayash
"High-efficiency fu
Meth. Enzymol. 303:
STRAIN-C57BL/6J; TISSUE-Testis;
Adachi J., Airawa K., Akimura T., Arakawa T., Bono H., Carninci P., Audochi J., Airawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; PubMed=110.78661; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.78661; DOI=10.1101/gr.152600;

Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

KONNO H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium, the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.",
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Testis; MEDLLNE=2049374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLLNE=2049374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a Nature 409:685-690(2001).
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C Q642A6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Von Willebrand factor A domain-related protein.
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SMART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44681 MW;
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EMBL; AK03
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SMART; SM00327; VWA; 1.
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EMBL; BC081983; AAH81983.1; -; mRNA.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
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Matches:
Conservative:
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ID Q4SCD1;
AC Q4SCD1
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                                                             US-10-699-035A-1 (1-537)
                                                                                                                                                            Percent Similarity:
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Anthouard C., Salanoubat M., Levy M., Boudet N., Castellano S.,
A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
A Anthouard V., Jubin C., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottler P., Coutanceau J.P., Gouzy J.,
A Cruaud C., Duprat S., Brottler P., Coutanceau J.P., Gouzy J.,
A Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Kindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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13-SEP-2005
13-SEP-2005
                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14659, whole genome sho
ORFNames=GSTENG00020556001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodo
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI TaxID=99883;
                                                                                                                                         Local Similarity:
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Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

M. Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

M. Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

M. Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

M. Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

M. Dasilva C., Sublin C., Castelli V., Katinka M., Vacherie B.,

M. Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

M. Biemont C., Skalli Z., Cattolicc L., Poulain J., De Berardinis V.,

M. Biemont C., Skalli Z., Cattolicc L., Ooutanneau J.P., Gouzy J.,

M. Biemont C., Skalli Z., Cattolicc P., Coutanceau J.P., Gouzy J.,

M. Biemont C., Jubin C., Cattolic P., Bosak S.,

M. Brara G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

M. Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

M. Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

M. Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

M. Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

M. Lindblad-Toh K., Birren B., Wusbaum C., Kahn D., Robinson-Rechavi M.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The Agarty, Vertabers of the Paractor of the Parac
NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an -!- CAUTION: The sequence shown here is derived from an -!-
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodo

Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF12445, whole genome s
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431:946-957(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003129; Laminin G_TSP
InterPro; IPR001220; Lectin legB.
InterPro; IPR001220; VWF A.
Pfam; PF01391; Collagen; 2.
Pfam; PF00041; fn3; 8.
Pfam; PF00092; VWA; 3.
Pfam; PF00092; VWA; 3.
PRINTS; PR000453; VWFADOMAIN.
SMART; SM00250; FN3; 9.
SMART; SM00250; TSPN; 1.
SMART; SM00327; VWA; 3.
PROSSITE; PS50853; FN3; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collagen;
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InterPro; IPR003961; FN_III.
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                                                                                                                                                                  GACGTGGATGACCTGCACATCATT 507
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                                                                                                                                                                                                                                                                                                                                                    GGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCC
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                                                                                                                             AsnValAlaAspPheHisLeuMet
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                                                                                                                                                                                                                                                                               ProAlaGlnArgLeuArgAspAlaGlyValGluValPheAlaIleGlyValLysAsnAla
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Query Match:
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NUCLEOTIDE SEQUENCE.

Authorn O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Anthouard V., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Parra G., Lardier S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-R
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SEQUENCE
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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SMART; SM00327; VWA; 3.
PROSITE; PS50853; FN3; 12.
PROSITE; PS50234; VWFA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00041; fn3; 11. Pfam; PF00092; VWA; 3.
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ORFNames=GSTENG00020231001;
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Chromosome 14 SCAF14645, whole genome shotgun sequence
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PRINTS; PR00453; VWFADOMAIN
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InterPro; IPR003962; FnIII_subd
InterPro; IPR002035; VWF_A.
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L; CAAE01014645; CAG01460.1; -;
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SerLeuValGlnTyrSerArgAspProHisThrGluPheTyrLeuAspSerHisHisAsn
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P32018; Q6LBLO;
01_JUL_1993 (Rel. 26,
01_OCT_1996 (Rel. 34,
13-SEP_2005 (Rel. 48,
                                                                                                                                                                 Apte S.S.;
Submitted
                                                                                                                                                                                                                 Van der Rest M., Mayne K., Vander Rest M., Mayne K., Vander Rember "Cloning of the cDNA for a new member sessociated collagens with interrupted associated collagens 201:333-338(1991).
                                                                                                                                                                                                                                                                               Gordon M., Castagnola P., Dublet B., L
van der Rest M., Mayne R., Olsen B.R.;
                                                                                                                                                                                                                                                                                                                                                     Trueb J., Trueb B.;
"Type XIV collagen is a variant of undulin.";
Eur. J. Biochem. 207:549-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen alpha 1(XIV)
Name=COL14A1;
 STRUCTURE
                                "Identification and characterization of a heparin binding site within the NC1 domain of chicken collagen XIV."; Matrix Biol. 17:145-149(1998).
                                                                                               MEDLINE=98357967; PubMed=9694594; Giry-Lozinguez C., Aubert-Foucher
                                                                                                  Giry-Lozinguez
                                                                                                                                    STRUCTURE
                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 1582-1770.
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92339443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93185668; PubMed=8444186; Waelchli C., Trueb J., Kessler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                   ВΥ
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 ВУ
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 NMR
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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Last annotation update)
chain precursor (Undulin).
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                                                                                                 DOI=10.1016/S0945-053X(98)90027-0;
E., Penin F., Deleage G., Dublet B.,
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triple helices.";
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-!- SUBCELLUAR LOCATION: Extracellular matrix.
-!- SUBCELLUAR LOCATION: Extracellular matrix.
-!- TISSUE SPECIFICITY: Wide tissue distribution; high presence in dense connective tissue in skeletal muscle.
-!- PTM: Lysines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in all cases and bind carbohydrates.
-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- PTM: May contain numerous cysteine residues involved in inter- and intramolecular disulfide bonding.
-!- SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.
-!- SIMILARITY: Contains 8 fibronectin type-III domains.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
-!- SIMILARITY: Contains 2 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen XIV by CD and NMR.",
Blockemistry 38:6479-6488(199).
-i- FUNCTION: An adhesive role by integrating collagen bundles. It is probably associated with the surface of interstitial collagen fibrils via COL1. The COL2 domain may then serve as a rigid arm which sticks out from the fibril and protrudes the large N-terminal globular domain into the extracellular space, where it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99280705; PubMed=10350466; DOI=10.1021/bi9900222; Montserret R., Aubert-Foucher E., McLeish M.J., Hill J.M., Jaquinod M., van der Rest M., Deleage G., Penin F.; "Structural analysis of the heparin-binding site of the NC:
s Swiss-Prot entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL Buropean Bioinformatics Institute. There are no restrict as long as its content is in no way modified and this state
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InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
Pfam; PP01391; Collagen; 4.
Pfam; PF00041; fn3; 8.
Pfam; PF00092; VWA; 2. EMBL; X70793; CAA50064.1; -; EMBL; X70792; CAA50063.1; -; EMBL; X66138; CAA46928.2; -; EMBL; X65122; CAA46238.1; -; PROSITE; PS50853; FN3; 8 PROSITE; PS50234; VWFA; ; X65122; CAA46238.1; A45974; A45974. S78476; S78476. 1B9P; NMR; A=1853-1885. 1B9Q; NMR; A=1853-1885. PR00453; VWFADOMAIN. Hydroxylation; Cell adhesion; FN3; 8. mRNA. mRNA. Collagen; Repeat; Si mRNA n; Extracellular matrix; Signal; Structural prot Structural protein

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Fibronectin type-III Fibronectin type-III

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Fibronectin

type-III

VWFA 1.

Collagen alpha 1(XIV)

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Potential.

Nonhelical region (NC4).
Triple-helical region 1 (COL2).
Triple-helical region 2 (COL1).
Cell attachment site (Potential).
Cell attachment site (Potential).

TSP VWFA

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Q4RP12 TETNG
Q4RP12;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 10 SCAF15009, whole genome shotgun seque
ORFNames=GSTENG00031322001;
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P. NUCLEOTIDE SEQUENCE.

A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

A Jaillon O., Aury J.M., Brunet F., Potit J.L., Stange-Thomann N.,

A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

A Nicaud S., Jaffe D., Fisher S., Boudet N., Castellano S.,

A Basilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

A Cruaud C., Jubin C., Castelli V., Katinka M., Vacherie B.,

A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

A Barra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Kellis M., Volff JN., Guigo R., Sauxin W., Scarpelli C.,

A Laudet V., Schachter V., Quetier F., Sauxin W., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

The early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
EMBL; CAAE01015009; CAG09870.1; -; Genomic_DNA.
SEQUENCE 1259 AA; 138606 MW; 844C01B6FE2D0E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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                                                    ---GACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATT
                                                                                                                                                                                                                 GluAspPheAspAlaPheGlnArgIleSerLysGluLeuThrGlnSerIle
                                                                                                                                                                       CCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGC
                                                                                                                                                                                                                                                     GGGGTGCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCC
                                                                                                                                                                                                                                                                                                                      GGCCTGGCGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCA
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                                                                                     ValArgSerGluLeuGluAlaIleAlaAsnProProAlaAspAsnHisValPheGluVal
                                                                                                   AACTICCTGGAGCTGTCAGCCGCTGCCAGCCCTGCCGAGAAGCACCTGCACTTTGTG
                                                                                                                                                     AlaAlaThrAsnLeuArgAsnIleAspValGluIlePheAlaValGlyValLysAspAla
                                                                                                                                                                                                                                                                                      GlyLysAlaMetLysTyrValLysAspLysIlePheValAlaSerArgGlyAlaArgGln
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RA Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M., Godin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., McTley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT and mouse cDNA sequences.",
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089029; 089030; Q99083;
16-OCT-2001 (Rel. 40, Last sequence up
10-MAY-2005 (Rel. 47, Last annotation
Matrilin-4 precursor (MAT-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT), AND VARIANTS.
STRAIN-C57BL/6J, and CD-1; TISSUE-Fetal;
MEDLINE-98442849; PubMed-9771906; DOI-10.1016/S0014-5793(98)01111-9;
MEGENER R., Kobbe B., Paulsson M.;
                   This Swiss-Prot entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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                                                                                                                                                                                                                                                                                                                                                                                                                                              human matri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 218-257.
MEDLINE=99043241; PubMed=9827539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagener R., Kobbe B., Paulsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Matrilin-4, a new member of
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic organisation, alternative splicing and primary structure of human matrilin-4.";
                                                                                                      TISSUE SPECIFICITY: Lung, brain, sternum, kidney and hear DEVELOPMENTAL STAGE: The short isoform was detected in 7 mice but not in developing mice (19.5 dpc embryos or in 2 ldays old animals).

21 days old animals).

SIMILARITY: Contains 4 EGF-like domains.

SIMILARITY: Contains 2 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Major component of the
                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                          Name=Short;
                                                                                                                                                                                                                                                                                                                    Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lett. 436:123-127(1998).
                                                                                                                                                                                                                                                                           IsoId=089029-1; Sequence=Displayed;
                                                                                                                                                                                                              IsoId=089029-2; Sequence=VSP_001401;
SSUE SPECIFICITY: Lung, brain, stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences."
1. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                    splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1016/S0014-5793(98)01293-9;
    way
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                                                                                                                                                                                                              sternum, kidney and heart.
                                                                                                                                                                                                                                                                                                                                                                                                       extracellular matrix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISOFORM LONG).
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                                                                                                                                                                                                       Query Match:
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Best Local Similari
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                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                    US-10-699-035A-1 (1-537) x MATN4_MOUSE (1-624)
                                                                                                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PÍAM; PF00008; EGF; 4.

PÉAM; PF000092; VWA; 2.

PIRSF; PIRSF015217; Matn vWA; 1.

PRINTS; PR00453; VWFADOMAIN.

PROSITE; PS01010; ASX HYDROXYL; 2.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS50126; EGF 3; FALSE_NEG
PROSITE; PS50234; VWFA; 2.

Alternative splicing; Colled coil;
                                                                                                                                                                                                                                                                                                                VARIANT
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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DOMAIN
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EMBL; AJ006140; CAA06890.1;
EMBL; BC036558; AAH36558.1;
EMBL; AJ010984; CAA09451.1;
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF-like.
InterPro; IPR011203; Matn_vMA.
InterPro; IPR002035; VWF_A.
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GO; GO:0005615; C:
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                                                                                                                                                                                                                                                                                    Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1328314; Matn4.
124
                                                                                                                                                                                                                       Similarity:
                             56
                                                           64
                                                                                          36
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                                                                                        AspLeuValPheMetIleAspSerSerArgSerValArgProPheGluPheGluThrMet
                                                        ceacaetrierececaecie
                                                                                                                         GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCG
                            ArgGlnPheLeuValGlyLeuLeuArgSerLeuAspValGlyLeuAsnAlaThrArgVal
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221
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36.8%
25.3%
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3; FALSE_NEG
                                                                                                                                                                                                                                                                                                                     WW.
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; -; mRNA.
; -; mRNA.
; -; Genomic_DNA.
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By sim
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EGF-like
EGF-like
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                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                    Conservative:
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 183
                               75
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COCA1 CHICK
ID COCA1 CHICK
ID COCA1 CAC
AC P13947;
DT 01-VAV-
DT 01-VAV-
DT 01-WAY-
DT 0
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                                                                                                  MEDLINE=87317590; PubMed=3476925;
Gordon M.K., Gerecke D.R., Olsen B.R.
"Type XII collagen: distinct extracel
by cDNA cloning.";
                                                                                                                                                                                                           "Type XII collagen. A large multidomain to type IX collagen.";
J. Biol. Chem. 264:19772-19778(1989).
                                                                                                                                                                                                                                                              Gordon M.K., Gerecke D.R., Dublet
                                                                                                                                                                                                                                                                                                                                                                                     "The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifs, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=White leghorn;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka
Nishida Y., Obara M., Kimata K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
 MEDLINE=93042014; PubMed=1420368; DOI=10.1016/0167-4781(92)90145-P;
                                                                                                                                                                                                                                                                                MEDLINE=90062079;
                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 2456-3124,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 2960-3076.
                                                                                                                                                                                                                                                                                                   AND 2846-2873
                                                                                                                                                                                                                                                                                                                                                      Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                              IX collagen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnArgAlaAspValGlySerLeuArgThrMetAlaSerProProLeuAspGlnHisVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValAlaGluValAlaAlaGlnAlaArgAlaArgGlyIleGluIleTyrAlaValGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyValIleGlnTyrSerSerGlnValGlnSerValPheProLeuGlyAlaPheSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                        115:209-221(1991).
                                                                                                                                                                                                                                                                                    PubMed=2584192;
                                                                                      Sci.
                                                     Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - GTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCT
                                                                                      U.S.A.
                                                     1-1283
                                                                                                                      extracellular matrix component discovered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                     (ISOFORM
                                                                                      84:6040-6044(1987)
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                                                     SHORT),
                                                                                                                                                                                                                                                 molecule
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                                                                                                                                                                                                                                               Rest M.,
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                                                     AND
                                                     ALTERNATIVE
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Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet "Large and small splice variants of collagen XII: differential expression and ligand binding.", J. Cell Biol. 130:1005-1014(1995).

-I- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrilar matrix.

-I- SUBUNIT: Trimer of identical chains each containing 190 kDa o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trueb J., "The two Biochim. [5]
                                                                          PRINTS, PRO0453; VWFADOMAIN.
SMART; SM00060; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D00824; BAA00701.1; -; mRNA.

EMBL; X61024; CAA4338.1; -; mRNA.

EMBL; M17375; AAA48718.1; -; mRNA.

EMBL; J05137; AAA48635.1; -; mRNA.

EMBL; X67327; CAA47744.1; -; mRNA.

EMBL; X67327; CAA47744.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and t
the European Bioinformatics Institute. There are no
use as long as its content is in no way modified and
                                                                                                                                                                            Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 17. Pfam; PF00092; WA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95370352;
Koch M., Bohrmann
                           PROSITE; PS50853; FN3; 18
PROSITE; PS50234; VWFA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE SPLICING
Alternative splicing; Cell adhesion; Collagen;
                                                                                                                                                                                                                                                                                                                                                                    Ensembl; ENSGALG00000015908;
                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                               nterPro;
                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the fibril-associated collagens interrupted helices (FACIT) family.
SIMILARITY: Contains 18 fibronectin type-III domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P13944-2; Sequence=VSP 001148; TISSUE SPECIFICITY: Type XII collagen is present in tendons ligaments, perichondrium, and periosteum, all dense connect tissues containing type I collagen.

DOMAIN: This sequence defines five distinct domains, two trhelical domains (COL1 and COL2) and three nontriple-helical domains (NC1, NC2, and NC3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. PTM: O-glycosylated; glycosaminoglycan of chondroitin-sulfate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
Comment=The final tissue form of collagen XII may co
homotrimers of either isoform Long or isoform Short
combination of isoform Long and isoform Short. Only
is a proteoglycan. Isoform Long has more restricted
in embryonic tissue than isoform Short;
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ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                     P56199;
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The triple-helical tail
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1391; Collagen; 4.
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L, Hagios C., Trueb B., Chiquet
of collagen XII: differential
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Triple-helical region (Comperfection, imperfection, Nonhelical region (NC2).
Triple-helical region (Comperfection)
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13-SEP-2005
13-SEP-2005
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63_TETNG
Q4SH63_7
NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead
Submitted (FEB-2004)
                                                                                         "Genome duplication the early vertebrate
                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Jaillon O., Aury J.N
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=99883;
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Jailon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Kallis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis (Green puffer).
Eukaryota; Mettazoa; Chordata; Cranitata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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ORFNames=GSTENG00018311001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  599 GluAspPheAspAlaPheGlnArgIleSerPheGluLeuThrGlnSerVal
                                                                                                                        r P., Lander E.S., Weissenbach J., e duplication in the teleost fish rly vertebrate proto-karyotype."; 431:946-957(2004).
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AspValValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheValLysVal
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(TrEMBLrel. 31, Last sequence upd
(TrEMBLrel. 31, Last annotation u
8 SCAF14587, whole genome shotgun
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RESULT 14
Q5VYKZ_HUMAN
ID Q5VYKZ_HUMAN PRELIMINARY;
AC Q5VYKZ;
DT 01-FEB-2005 (TremBLrel. 29,
DT 01-FEB-2005 (TremBLrel. 29,
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SMART; SM00060; FN3; 6.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 2.
PROSITE; PS50853; FN3; 7.
PROSITE; PS50234; VWFA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen;
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Pfam; PF00041; fn3; 6.
Pfam; PF00092; VWA; 2.
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InterPro; IPR003961; FM_III.
InterPro; IPR003295; Laminin_G_TSP_N.
InterPro; IPR002035; VWF_A.
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                                                                                                                1031 AlaAspTyrGlyGluLeuValAsnIleAlaSerLysProSerAspArgHisValPhePhe
                                                                                                                                                         1011 LysValSerLysGluMetGlnMetAspGlyTyrIleIlePheAlaIleGlyPheAlaAsp
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                                                                                                                                                                                                                      CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC
                                                                                                                                                                                                                                                                                                                        ValAlaIleAlaGlnPheSerAspAspAlaArgThrGluPheGlnLeuSerSerHisSer
                                                                                                                                                                                                                                                                                                                                                GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                GACCTGATGTTCCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
                                                                        ||| || || ::::|| | || ::::||| valAspAspLeuAspAlaValLysLysIleGluGluGlnLeu
                                                                                                                                                                                                                                       ACTGGCCTGGCGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
                                                                                                                                                                                                                                                                                asnLysGluAlaLeuLeuGluAlaIleGlnLysIleSerTyrLysGlyGlyAsnThrLys
                                                                                                                                                                                                                                                                                                       TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCGTTCTGCCCAGCGCATGGGTGACACCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                           AspLeuValPheLeuValAspGlySerTrpSerIleGlyAspGluAsnPheMetLysIle
                                                                                                                                    GGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCGAGAAGCACCTGCACTTT
                                                                                                                                                                             CCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1557 AA; 168266 MW;
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56.3%
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EMBL; AL354664; CAH71309.1; -; Genomic_DNA.

EMBL; AL080250; CAH19897.1; -; Genomic_DNA.

EMBL; AL080771; CAH71309.1; -; Genomic_DNA.

EMBL; AL096771; CAH71309.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH71309.1; JOINED; Genomic_DNA.

EMBL; AL354664; CAH19897.1; JOINED; Genomic_DNA.

EMBL; AL354664; CAH19807.1; JOINED; Genomic_DNA.

EMBL; AL354664; CAH19907.1; JOINED; Genomic_DNA.

EMBL; AL354664; CAH19907.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH19807.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH19807.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH19807.1; JOINED; Genomic_DNA.

EMBL; BL096771; CAH19807.1; JOINED; Genomic_DNA.

EMBL; BL096771; CAH19807.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:000578; C:extracellular matrix (sensu Metazoa); IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0007155; P:phosphate transport; IEA.
InterPro; IPR00310; COllagen.
InterPro; IPR00319; IAminin_G_TSP_N.
InterPro; IPR00319; LAminin_G_TSP_N.
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Collagen, type XII, alpha 1.
Name=COL12A1; ORFNames=RP1-238D15.1-003;
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50853; FN3; 18.
PROSITE; PS508234; VWFA; 4.
Collagen; Extracellular matrix;
SEQUENCE 2884 AA; 315869 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00453; VWFADOMAIN. SMART; SM00060; FN3; 18. SMART; SM00210; TSPN; 1. SMART; SM00327; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 18. Pfam; PF00092; VWA; 4.
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                                                                                            ArgAlaPheLeuGluValLeuValLysSerPheGluIleSerProAsnArgValGlnIle
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                                             AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG
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2D598F13656E454D CRC64;
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Matches:
Conservative:
Mismatches:
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COS715; COS716;

COS715; COS716;

15-JUL-1998 (Rel. 36; 1

15-JUL-1998 (Rel. 36; 1

10-MAY-2005 (Rel. 47; 1
                                                                                                                                                                                                                                                                                                MEDLINE=97288521; PubMed=9143499; DOI=10.1006/geno.1997.4638; Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R., Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.; "Complete primary structure of two splice variants of collagen and assignment of alpha 1(XI) collagen (COL12A1), alpha 1(XX)
                                                                                                                                                                                                                                                                 collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human chromosome 6q12-q13.";
Genomics 41:236-242(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen alpha 1(XII)
Name=COL12A1;
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                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND
                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
  carcinoma cell line.
- PTM: The triple-helic
each end (By similar:
- PTM: Prolines at the
                                         IsoId=Q99715-2; Sequence=VSP_001149;
TISSUE SPECIFICITY: Found in collagen I-containing tissues: both isoform Short and isoform Long appear in amnion, chorion, skeletal muscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the short isoform is found in lung, placenta, kidney and a squamous cell
                                                                                                                                           Event=Alternative splicing, Named isoforms=2;
Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or an
combination of isoform Long and isoform Short;
                                                                                                                                                                                                             localized in the perifibrillar matrix (By similarity) SUBUNIT: Trimer of identical chains each containing 1
                                                                                                                                                                                                                                 FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with surface of the fibrils, and the COL2 and NC3 domains may be
                                                                                                             Name=Short
                                                                                                                                                                                        nontriple-helical sequences.
ALTERNATIVE PRODUCTS:
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                                                                                                                        IsoId=Q99715-1; Sequence=Displayed;
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                      triple-helical tail is stabilized
            (By similarity)
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 the third position
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Last annotation update)
chain precursor.
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InterPro; IPRO08160; Collagen.
InterPro; IPRO03961; FN III.
InterPro; IPRO02035; VWF A.
Pfam; PF001391; Collagen; 4.
Pfam; PF00091; fn3; 18.
Pfam; PF00092; VWA; 4.
PRINTS; PR00453; VWFADOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing; Cell adhesion; Direct protein sequencing; Extracellusydroxylation; Perce
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GO; GO:0001501;
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EMBL; U73779; AAD40483.1;
HSSP; P18614; 1MHP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydroxylation; Repeat; Signal; Structural protein
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SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unit (G-X-Y) are hydroxylated in some or all of the chasimilarity).

PTM: 0-glycosylation of isoform Long; glycosaminoglycan
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Bioinformatics Institute.
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P:skeletal development;
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                      Triple-helical region (COL1) with imperfections.

Nonhelical region (NC1).

Cell attachment site (Potential)

Cell attachment site (Potential)

Cell attachment site (Potential)
Hydroxyproline Hydroxyproline
                                                                                                                  Nonhelical region
Triple-helical reg
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Fibronectin type-III 1.
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AspIleValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheValLysVal
GluAspPheAspAlaPheGlnArgIleSerPheGluLeuThrGlnSerIle
                               ---GACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATT 531
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Search completed: February 13, 2006, 13:38:53 Job time : 147.574 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd

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ALIGNMENTS

RESULT 1 AAE32500 ID AAE3 Misc-difference 1. .2 gene willebrand Factor A domain related-protein; extracellular matrix; ECM; molecular marker; Human von Willebrand Factor A (VA) domain. AAE32500; 07-NOV-2002 WO200288184-A1 Misc-difference 179. .180 24-MAR-2003 (first entry) AAE32500 standard; protein; 180 AA Homo sapiens. therapy; human. /note= "Encoded by CTC" note= "Encoded by GGG" von Willebrand Factor A; VA; ; cartilage; arthritis; WARP;

Bateman JF,

Fitzgerald DJ;

02-MAY-2002; 2002WO-AU000542

02-MAY-2001; 2001AU-00004701

(MURD-) MURDOCH CHILDRENS RES INST.

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                        GTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTC 534
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The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human VA domain New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis. Claim 7; Page 72-73; 103pp; English. N-PSDB; 2003-111873/10. DB; AAD50397.

4.51e-69 902.00 100.0% 100.0% 86.0% Length: Matches: Conservative: Mismatches: Indels:

180 178 0 0

x AAE32500 (1-180)

AAB87344 standard; protein;

AAB87344;

22-MAY-2001 (first entry)

Human gene 3 encoded secreted protein HNTEO78, OI DES NO:85

Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification. Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; rheumatoid; allergy; neurological disorder; Alzheimer's disease;

Homo sapiens.

WO200118022-A1

15-MAR-2001

31-AUG-2000; 2000WO-US024008

03-SEP-1999; 03-SEP-1999; 99US-0152315P. 99US-0152317P.

(HUMA-) HUMAN GENOME SCI INC.

Soppet PA, Baker KP, DR, Young Young Shi Y, Birse CE, Fiscella M, PE, Ebner R, Duan DR, Wei Y, Florence KA; Komatsoulis GA, Rosen CA; Olsen HS, Lafleur DW;

2001-203081/20.

Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.

Claim 11; Page 532-533; 607pp; English.

CC AAB971858-AAF91929 represent cDNAs corresponding to 52 human secreted CC protein genes, and AAB8742-AAB87411 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes can their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating the protein in a sample or by determining the protein of the creating of the mean protein in a sample or by determining the presence of creating the discorders, can described for each of the creating of the mutations in the new genes. Specific uses are described for each of the creating discorders, cancer, tumours, foetal and developmental creating discorders, schizophrenia, asthma, skin creating cancer, tumours, foetal and developmental creating discorders, schizophrenia, asthma, skin creating and epithelial cell proliferation, to prevent skin aging due to consist and developmental cell proliferation, to prevent skin aging due to consist and developmental cell proliferation, to prevent skin aging due to consist a load and can be used in discorders specific for a protein of the invention can be used in alleviating symptoms associated with the discorders mentioned above, and can be used can be used can decordered protein of the invention can be used in munosorbent assay (ELISA). The present sequence represents a human created protein of the invention

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                                                                                                                                                              immunomodulator; anti-HIV; antidiabetic; haemosta
neuroprotective; antiparkinsonian; antimicrobial;
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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                                                                                   The invention relates to a novel albumin fusion protein. The invention CC further relates to: a composition comprising the albumin fusion protein CC and a pharmaceutical carrier; a kit comprising the composition of the CC albumin fusion protein formula; a method of treating a disease or CC disorder in a patient comprising the steep of administering the albumin CC fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; CC fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; and a host cell CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The cCC comprision protein and its compositions have the following CCC dermatological, antipout, immunomodulator, antiarrhythmic, CCC dermatological, antipout, immunomodulator, antiarrhythmic, CCC cardiant, nootropic, antilipaemic, nephrotropic, uropathic, anabolic, antiparkinsonian, tranquilizer, antidiabetic, anabolic, and transport to antiparking fusion protein antiarrhythmic and uniterary.
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immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic;
hypertensive, and vulnerary. The albumin fusion protein nucleic acid make used in gene therapy to treat disorders. The albumin fusion protein useful for diagnosing, treating, preventing or ameliorating diseases or disorders comprising indication: Y. The diseases or disorders include:
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CC disease), reproductive system disorders (e.g. prostatilis, inguinal CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertolic leydig tumours), musculoskeltaid diseases (e.g. giant cell tumours, CC leydig tumours), musculoskeltaid diseases (e.g. giant cell tumours, CC archexia), cardiovascular disease (e.g. rhabdomyomas, heart disease, CC arrhythmia, cardiovascular disease (e.g. foetal alcohol syndrome, CC arrhythmia, mixed foetal diseases (e.g. foetal alcohol syndrome, TC Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay CC Sachs disease, parkinson's diseases (e.g. urinary incontinence, urinary CC tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, parkinson's disease, cerebral malaria, meningitis, CC cerebellar ataxia, attention deficit disorder, autism or obsessive CC compulsive disease), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine disease (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal CC disease or glomerulonephritis), digestive diseases (e.g. portal CC connective tissue or epithelial diseases (e.g. Crohn's disease, CC seleventes at therapeutic protein x relating to the albumin fusion protein confict in invention. The sequence listing data for this specification was considered the disease of the superior was specification was considered the disease of the superior considered form the USPTO website. lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS, autoimmune disease, inflammatory bowel disease, psoriasis or Lyme cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute

Sequence 215 8

Percent Similarity:

No.:

á Ş 밁 Ś 밁 S 밁 S 밁 Ş 밁 Ş 밁 Ś 밁 Ş 밁 US-10-699-035A-1 (1-537) x ADL78614 (1-215) Query Match: Best Local Similarity: 481 173 421 153 361 133 301 113 241 193 181 121 93 73 53 61 Ü GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC CCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA ProGlyValProLysValLeuValTrpValThrAspGlyGlySerSerAspProValGly AlaSerLeuValHisValGlySerArgProTyrThrGluPheProPheGlyGlnHisSer GTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGT GlyAspLeuMetPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArg GGGGACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCCGG CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCAC ProProMetGlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGlyArg 4.68e-69 902.00 100.0% 100.0% 86.0% .yGlnLeuValAlaProLeuProLeuGl Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 215 178 0 0 0 534 210 480 132 112 172 152 360 300 240 92 180 72 52 192

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CC AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted CC protein genes, and AAB87342-AAB87413 represent the proteins they encode. CC AAB87414-AAB87454 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the C2 genes, based on the tissues in which they are most highly expressed, CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, disease of the immune system, CC parkinsons's diseases (e.g., Alzheimer's disease, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC gastrointestinal disorders, pregnancy-related disorders, abcorders, endocrine CC disorders, and epithelial cell proliferation, for supporting due to sunburn, to maintain organs before transplantation, for supporting cell cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC cantibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing, treating or ameliorating Parkinson's diseases and cancers.
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          Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; inmune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gendocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
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CC Antibodies specific for a protein of the invention can be used in disgnostic immunoassays e.g., radioimmunoassay erepreties a human cc secreted protein fragment referred to in the discorders a human cc secreted protein fragment referred to in the discorder of the invention
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03-SEP-1999;
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                    GTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGT
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11-JAN-2000;
02-MAY-2000;
AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can
                                                       which encode human secretory or membrane proteins represented by AAB88 - AAB88419. Included in the invention are primers AAF93917 - AAF94295
                                                                                                                                                                      Nucleic acids encoding secretory proteins/membrane gene therapy or as candidate target molecules in dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
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                                                                                             This invention relates to nucleic acid sequences AAF93744 -
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02-MAY-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
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                                                                                              w isolated Willebrand Factor A-Related Protein polypeptide useful for e manufacture of a medicament in the treatment of a disease condition the extracellular matrix, in particular arthritis.
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                                               103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human mature WARP protein"
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invention

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Willebrand Factor A

domain related-protein

TXXXXXXXXXXXXX

ABP69674

standard;

protein;

Human polypeptide SEQ ID NO

1721.

(first

entry)

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection multiple sclerosis; diabetes; genetic disorder; wound; burn; infections;

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human WARP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 418
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                                                                                                           CCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA
                                                                                                                                              ProGlyValProLysValLeuValTrpValThrAspGlyGlySerSerAspProValGly
                                                                                                                                                             CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC
                                                                                                                                                                                             ThrGlyLeuAlaLeuValTyrAlaLysGluGlnLeuPheAlaGluAlaSerGlyAlaArg
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                                                                                                                                                                                                                                                                                                                                            GlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPhe
                                                                                                ProProMetGlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGlyArg
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US-10-699-035A-1 (1-537) x ABP69674 (1-445)
                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                          mucleotide sequence selected from any of 948 sequences (ABZIII9)

CA ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for cidentifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68992-ABP69849) are useful as molecular weight comarkers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-complificative disorders (cancer), neurodegenerative diseases (Parkinson's complificative disorders (cancer), neurodegenerative diseases (Parkinson's complification disorders, myeloid or lymphoid disorders, liver complities, infections (bacterial, viral, fungal, parasitic), complities, etc. Note: The sequence data for this patent did not form part compliance of the printed specification, but was obtained in electronic format complex contents.
                                                                                                                                                                                                                                                                                                Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 1721; 1012pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative, autoimmune, genetic,
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T, Wang J,
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                                                                                              ValArgGluPheValGlyGlnLeuValAlaProLeuProLeuGlyThrGlyAlaLeuArg
   TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCCAC
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Ma Y, Yamazaki V, Chen R,
, Wang D, Drmanac RT;
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05-JUN-2002;
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2002US-0386796P.
2002US-0386816P.
2002US-0386931P.
2002US-0386971P.
2002US-0387262P.
2002US-0387400P.
2002US-0387635P.
2002US-0387634P.
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2002US-0386376P.
2002US-0386453P.
2002US-0386864P.
2002US-0387016P.
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18-JUN-2002
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09-AUG-2002
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113-AUG-2002
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                                                                                                                                                                                                                                                                  Rieger DK,
Smithson G,
Zhong H;
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Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
Paddigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
                                                                                                                  treating
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                                                                                                                                                                                               ADH71105.
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                                                                                         polypeptides and nucleic acid molecules useful for preventing NOVX-associated disorders, e.g. cancer, diabetes, infection or and in chromosome mapping, tissue typing or pharmacogenomics.
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2002US-038802EP.
2002US-038802EP.
2002US-038802EP.
2002US-038912EP.
2002US-038912EP.
2002US-038912EP.
2002US-038914EP.
2002US-038914EP.
2002US-0389742P.
2002US-0399762P.
2002US-0399762P.
2002US-0399762P.
2002US-0402156P.
2002US-0402156P.
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2002US-0402156P.
2002US-0402156P.
2002US-0402156P.
2002US-040351P.
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2002US-040353P.
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2002US-041484P.
2002US-042269P.
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2002US-042269P.
2002US-042269P.
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Example 1; SEQ

ID NO

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1880pp; novel

English. isolated

polypeptide

matrix and

cell adhesion molecule-18

(XMAD-18).

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Best Local Similarity:
Query Match:
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06-AUG-2001
                          AAE03654;
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                                                     standard;
                                                                                                                                                               GlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPhe
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entry)
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Mismatches:
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Gaps:
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inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; extracellular matrix and cell adhesion molecule; XMAD; gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
neuroprotective; dermatological.
                                                                 arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephrotropic;
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Homo sapiens

Region /note= "Von Willebrand factor note= Location/Qualifiers note= . 170 . 51 "Collagen glycoprotein "Collagen "Collagen glycoprotein precursor" "Collagen glycoprotein glycoprotein precursor" precursor" precursor" domain score"

WO200142285-A2

05-DEC-2000; 2000WO-US032990

10-DEC-1999; 16-DEC-1999; 99US-0172852P 99US-0172354P

INCYTE GENOMICS INC.

₩. Tang . Lu f DAM, Lal P Shah Burford N, Azimzai Y, P, Au-Young J; Au-Young Patterson ü

WPI; 2001-381632/40

New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative disorders.

Claim 1; Page 111; 135pp; English

cc polynucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally clethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders cassociated with expression of XMAD. They are also used for generating hybridisation probes useful in mapping the naturally occurring genomic sequences and to create knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human diseases. Oligonucleotide or longer fragments derived from the polynucleotide sequences may be used as celements on a microarray. Antibodies which specifically bind XMAD may be used for the diagnosis of disorders associated with the expression of CC windows of the polynucleotide genetic disorders such as addinated prevented or treated include genetic disorders such as addinated in prevented in the specifically bind XMAD. Diseases colleges, myotonic dystrophy, sickle cell anaemia, thalassaemia, attender, antipolical disports affords a argenia attended the control of the control of the control of the control of the colleges and the colleges argenia attended the colleges and the colleges argenia attended the colleges and the colleges argenia attended the col The present sequence is a human extracellular matrix and cell adhesion molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonior antagoinst are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The Crohn's disease, diabetes allergies, anaemia, asthma dermatitis agonist

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthr. osteoporosis, psoriasis, rheumatoid arthritis, ulcerative collitis, bacterial, fungal, parasitic, protozoal and helminthic infections at cell proliferative disorders such as actinic keratosis, arterioscle: and cancer including breast, bladder, bone marrow, brain and uterus
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GlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGlyArgGlyAsnPhe
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                                                                     CTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTG
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                                                                                                                                                                                                                                            GCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTG
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                                                      LeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPheValAspVal
                                                                                                                                    CAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACTTC
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886.00
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AAB42581 protein;

(first entry

Human ORFX ORF2345 polypeptide sequence SEQ ID NO:4690

ARBSULT 13
AAB42581
ID AAB42
XX AAB42
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XX AAB42
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XX Humar
XX Vulne
KW Vulne
KW Immur
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KW Antick
KW Antick Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antirinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension, antianaemic; gene therapy; cancer; proliferative disorder; hypertension. antianaemic; gene therapy; cancer; neurodegenerative disorder; osteoa graft hypertension; cardiant;

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                                                                                                                                                                                                                                                                                                                             Sequence 299
                                                                                                                                                                                                                                                                                                                                                            disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 3880-3881; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
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05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC74446 to AAC77606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-)
                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                   Match:
                                                                                                                                                                                                                                                                                           Scores
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 57
                                 64
                                                                         37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽,
                                                                                        GACCTGATGTTCCTGCTGGACAGCCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCCGGGTT
CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCC
                                                                       AspLeuMetPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; cartilage damage; antiinflammatory disease; coagulation; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-00540763
                                                                                                                                                                                                                                                                                                                             ₽,
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99US-0127728P.
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877.00
98.3%
98.3%
83.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encode the proteins given in AAB40237 to AAB43397,
                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                Indels:
Gaps:
                                                                                                                                                                              299
174
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                                                                                                            WPI; 200
N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                  gene
                                                                New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                                                                             Willebrand Facextracellular
                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE32503
                                                                                                                                              Bateman
                                                                                                                                                                                         02-MAY-2001;
                                                                                                                                                                                                                02-MAY-2002; 2002WO-AU000542
                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE32503;
                                                                                                            2003-111873/10.
DB; AAD50400.
                                                                                                                                                                                                                                                                                                                                                 therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484
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                                                                                                                                                                    MURDOCH CHILDRENS RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCG
                                           Page 78-79; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein; 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspValAspAspLeuHisIleIleValGlnGluLeuArgGlySerIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerLeuValHisValGlySerArgProTyrThrGluPheProPheGlyGlnHisSerSer
                                                                                                                                                                                                                                                                                                                                                                                               Willebrand
                                                                                                                                                                                                                                                                                                                                                             Factor A domain lar matrix; ECM;
                                                                                                                                             Fitzgerald
                                                                                                                                                                                         2001AU-00004701
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                    mouse.
                                                                                                                                                                                                                                                                                                                                                            matrix;
                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .2
                                                                                                                                                                                                                                                                                                                                                                                               Factor
                                                                                                                                                                                                                                                                                  "Encoded by GGG"
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                                                                                                                                                                                                                                                                                                                                                             related-protein; von Willebrand Factor A; VA; molecular marker; cartilage; arthritis; WARP;
                                                                                                                                                                                                                                                                                                                                                                                              A (VA) domain.
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The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain prosuperfamily of extracellular matrix (ECM) proteins. WARP is used as

-domain protein
 is used as a

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RESULT 1
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Query
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Pred. No.:
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y Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is mouse VA domain
                                                             Willebrand Factor A domain related-protein; von Willebrand Factor A; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WJ
                                                                                                                 Mouse
                                                                                                                                                 24-MAR-2003
                                                                                                                                                                                                               AAE32501
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                                              therapy;
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                                                                                                                                                                                                                                                                                                                                               142
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                                                                                                               Willebrand
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                                                                                                                                                                                                                 standard;
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                                                                                                             Factor A domain related-protein
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762.00
91.5%
84.2%
72.6%
                                                                                                                                                                                                             protein;
                                                                                                                                               entry)
                                                                                                                                                                                                                 415
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Matches:
Conservative:
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                                                                 A; VA;
WARP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to Willebrand Factor A domain related-protein (MARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is mouse WARP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Willebrand Factor A-Related Protein polypeptide useful the manufacture of a medicament in the treatment of a disease condit of the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 74-75; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                            GlyAspLeuLeuPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArg
                                                                                                                                                                                                                                                                                                                                                                                                          Å
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Search completed: February 13, 2006, 13:23:30 Job time : 97.9481 secs

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Result
No.
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Ygapop 10.0 , Ygapext
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US-10-699-035A-2

US-09-789-561-85

US-09-833-245-2096

US-10-883-936-85

US-09-789-561-165

US-09-789-561-159

US-09-789-561-159

US-10-883-936-159

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                                Sequence 2, Appli
Sequence 85, Appl
Sequence 2096, Appl
Sequence 165, Appl
Sequence 165, Appl
Sequence 169, Appl
Sequence 159, Appl
Sequence 5, Appli
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Sequence 6, Appli
Sequence 20, Appli
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RESULT 1 US-10-699-035A-2

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Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Bizzgerald, David
ITITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699.035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
US-10-699-035A-1 (1-537) x US-10-699-035A-2 (1-180)
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                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 40 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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TYPE: PRT
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Matches:
Conservative:
                                                              Mismatches:
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Sequence

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1 GGGGACCTGATGTTCCTGCTGGACAGCCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCCGG

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
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                                                                                                                                                               NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION:
US-09-789-561-85
                                                                                                          Score:
                                                                                                                        Pred. No.:
                                                                                                                                     Alignment Scores:
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 85
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ORGANISM: Homo sapiens
FEATURE:
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US-10-699-035A-1 (1-537) x US-09-833-245-2096 (1-215)
                                          Query Match:
                                                                                                   Pred. No.:
                                                                                                                 Alignment Scores:
                                                                                                                                               US-09-833-245-2096
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 2096
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2096, Application US/09833245 Publication No. US20040010134A1 GENERAL INFORMATION:
                                                                                                                                                         FEATURE:
NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: J
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Human Genome Sciences, Inc. TITLE OF INVENTION: Albumin Fusion Proteins FILE REFERENCE: PF546PCT
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; OTHER INFORMATION:
US-10-883-936-85
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US-10-883-936-85
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                                                             Score:
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CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
                                                                          Pred. No.:
                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 85, Application US/10883936
Publication No. US20050019866A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 85
LENGTH: 215
                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                NAME/KEY: SITE
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               Conservative: Mismatches: Indels:
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Matches:
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APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted prote
FILE REFERENCE: PZ043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-09-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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US-09-789-561-165
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Best Local Similarity:
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US-10-699-035A-1 (1-537) x US-09-789-561-165 (1-226)
                                             Query Match:
                                                                                                                      Alignment Scores:
                                                                                                                                                   US-09-789-561-165
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                                                                                                        Pred. No.:
                                                                                                                                                                SOFTWARE: Patent
SEQ ID NO 165
LENGTH: 226
TYPE: PRT
ORGANISM: Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165, Application Patent No. US20020064818A1
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SOFTWARE: PatentIn Ver.
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OS: 194
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                                           Length:
Matches:
Conservative:
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FILE DEFENENCE: PZG43P1

CURRENT APPLICATION NUMBER: US/10/883,936

CURRENT FILING DATE: 2004-07-06

PRIOR APPLICATION NUMBER: US/99/789,561

PRIOR FILING DATE: 2001-02-2

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: BCT/US00/24008

PRIOR APPLICATION NUMBER: G0/152,317

PRIOR APPLICATION NUMBER: 60/152,317

PRIOR FILING DATE: 1999-09-03

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 194

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 165

LENGTH: 226

TYPE: PRT

ORGANISM: Homo sapiens
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US-10-883-936-165
; Sequence 165, A
                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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                              US-10-699-035A-1 (1-537) x US-10-883-936-165 (1-226)
                                                                                                                                            Alignment Scores:
                                                                                                                                                                         US-10-883-936-165
                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20050019866A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
                                                                                                                                No:
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D. US20050019866A1
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Matches:
Conservative:
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 159
LENGTH: 242
TYPE: PRT
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US-09-789-561-159
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     Percent Similarity:
                 Score:
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                                           Alignment Scores:
                                                                          US-09-789-561-159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 159, App
Patent No. US200
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
                                                                                                                                                                                    FEATURE:
NAME/KEY: SITE
LOCATION: (2)
                                                                                      NAME/KEY: SITE LOCATION: (34) OTHER INFORMATION:
                                                                                                                                           OTHER INFORMATION:
NAME/KEY: SITE
LOCATION: (5)
                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                               ORGANISM: Homo
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Length:
Matches:
Conservative:

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Best Local Si
Query Match:
DB:
                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-08-317
PRIOR APPLICATION NUMBER: G0/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 159
LENGTH: 242
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US-10-883-936-159
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 159, Application US/10883936 Publication No. US20050019866A1 GENERAL INFORMATION:
ORGANISM: Homo sapiens FEATURE: NAME/KEY: SITE LOCATION: (2) OTHER INFORMATION: Xaa FEATURE: NAME/KEY: SITE LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 52 Human secreted proteins FILE REFERENCE: PZ043P1
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                                                                                                                                     TYPE: PRT
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APPLICANT: Bateman, John
APPLICANT: Pitzgerald, David
ITITLE OF INVENTION: A Molecular Marker
ITITLE OF INVENTION: A Molecular Marker
ITITLE OF INVENTION: A Molecular Marker
ITITLE OF INVENTION: WIMBER: US/10/699,035A
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AD PRA701/01
PRIOR APPLICATION NUMBER: AD PRA701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 418
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Best Local Similarity:
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FEATURE:
NAME/KEY: SITE
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APPLICANT: Bateman, John

APPLICANT: Fitzgerald, David

APPLICANT: Fitzgerald, David

FITZ FOR INVENTION: A Molecular Marker

FILE REFERENCE: A36056 PCT USA A 071838.0142

CURRENT APPLICATION NUMBER: US/10/699,035A

CURRENT FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: PC7/AU02/00542

PRIOR FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR FILING DATE: 2001-05-02

NUMBER OF SEG ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SSEQ ID NO 20
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US-10-699-035A-20
is Sequence 20, Application US/10699035A
publication No. US20040214349A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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                    US-10-699-035A-20
                             LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: INCYTE GENOMICS,
APPLICANT: YUE, Henry
APPLICANT: YUE, Henry
APPLICANT: AZIMZAL, Yalda
APPLICANT: PATTERSON, Chandr
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: SHAH, Purvi
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
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US-10-149-819-18
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Best Local Similarity:
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  TYPE: PRT
ORGANISM: Homo
                    LENGTH: 185
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US-10-699-035A-1 (1-537) x US-10-699-035A-20 (1-418)
CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 18
                                                                                                                                                                                                                                                                                            Sequence 18, Application US/10149819
Publication No. US20030044913A1
                                                                                                APPLICANT: SHAH, Purvi
APPLICANT: LAL, Preeti
APPLICANT: AU-YOUNG, Janice
APPLICANT: BURFORD, Neil
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND
FILE REFERENCE: PF-0760 PCT
                                                                                                                                                                                                                                                                                                                                                               CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCCAGCGACCCTGTGGGC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
APPLICANT: Fitzgerald, David
FITTE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/ANU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR PILING DATE: 2001-05-02
INUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity:
Query Match:
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US-10-699-035A-8
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte
US-10-149-819-18
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10-699-035A-8
          LENGTH: 180
TYPE: PRT
ORGANISM: Mus musculus
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RESULT 13

US-10-699-035A-31

; Sequence 31, Application US/10699035A

; Publication No. US20040214349A1

; GENERAL INFORMATION:

APPLICANT: Bateman, John

APPLICANT: Fitzgerald, David

TITLE OF INVENTION: A Molecular Marker

FILE REFERENCE: A36056 PCT USA A 071838.0142

CURRENT APPLICATION NUMBER: US/10/699,035A

; CURRENT FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: PCT/AU02/00542

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR APPLICATION NUMBER: US/10/699,035A

CURRENT FILING DATE: 2001-05-02

; PRIOR FILING DATE: 2001-05-02

; NUMBER OF SEQ ID NOS: 40

; SOFTMARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 181
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Percent Similarity:
Best Local Similarity:
Query Match:
; OTHER INFORMATION: US-10-699-035A-31
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                                TYPE: PRT
ORGANISM: Artificial Sequence
                         FEATURE:
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Alignment Scores:

92 180 72 52

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Best
                                                                                     ; SEQ ID NO 4
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-699-035A-4
                                                                                                                                                         APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
FURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-699-035A-4
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                                                                                                                                              APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-3
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR PILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
IPRIOR FILING DATE: 2001-05-02
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 415
TYPE: PRI
ORGANISM: Mus musculus
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Search completed: February 13, 2006, 13:53:23 Job time : 91.701 secs
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-MODEL=frame+_n2p.model -DEV=xlp
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-LIST=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p -USER=US10699035 @CGN 1 1010 @runat 13022006 062447 25513 -NCFU=5 -NO_MAAP -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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US-09-907-794A-34

US-09-905-125A-34

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equence	ence 2	equence 2:	equence 2:	equence 22	e 9,	equence 6,	equence 1,	equence 2,	equence 98	equence 6	equence 27	35	36	7	34	1,	11	1, Appl	equence 4, Appl	equence 1, Appl	equence 37, App	quence 3	equence 3, Appl	equence 11520,	equence 11519,	equence 6215, A	equence 34, App	nce 34,	e 34, App	equence 34, App	quence 34, App	equence 34,

ALIGNMENTS

RESULT 1 US-09-513-999C-6277

Sequence 6277, Application US/09513999C Patent No. 6783961

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Query Match:
DB:
                                                                   Percent Similarity:
Best Local Similarity:
US-10-699-035A-1 (1-537) x US-09-513-999C-6277 (1-77)
                                                                                                                    Pred. No.:
                                                                                                                                      Alignment Scores:
                                                                                                                                                                    ; OTHER INFORMATION: US-09-513-999C-6277
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6277
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                            LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                     FEATURE:
NAME/KEY: UNSURE
LOCATION: 66
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                                     2.51e-26
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98.7%
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Matches:
Conservative:
Mismatches:
Indels:
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527 531 507 474 487 414 467

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Query Match:
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; ORGANISM: Human
US-09-949-016-10340
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-949-016-10340
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LENGTH: 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
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Best Local Similarity:
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PRIOR FILING DATE: 2000-10-20
PRIOR PEPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10341
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Patent No. 681233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                            124 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG
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                                           GlyLeuAlaLeuArgHisMetValGluHisSerPheSerGluAlaGlnGlyAlaArgPro
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CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
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Patent No.
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ZIP: 943
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                          LysGluPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal 96
                                                                                                         GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
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3174 Porter Drive
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Shah, Purvi
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APPLICANT: Wood, William, I...

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTE 1001-07-17

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Stewart, Timothy A.
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PRIOR FILING DATE: 1999-12-02

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PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: PCT/US99/30095

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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30995
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999
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CURPERT ADDITION: ACIDS ENCODING the Same
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                APPLICATION NUMBER: PCT/US00/00219 FILING DATE: 2000-01-05
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Williams, P. Mickey
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Hillan, Kenneth, J.
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Botstein, David
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art, Timothy A.
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APPLICANT: Ashkenazi,
APPLICANT: Botstein,
APPLICANT: Desnoyers,
APPLICANT: Eaton, Dan
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LENGTH: 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                217 PheLeuValAlaAsnPheSerGlnIleGluThrLeuThrSerValPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 GlyGlnValAspPheAsnThrLeuLysSerIleGlySerGluProHisGluAspHisVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LysSerGluValGluArgAlaValLysArgMetArgHisLeuSerThrGlyThrMetThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCCTGCGTGCC
                                                                                                                       Fong, buc...
Gao, Wei-Qiang
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Gurney, Austin L.
Hillan, Kenneth, J.
                                 Godowski, Paul J.
Grimaldi, Christopher
                                                                                            Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                          Ferrara, Na
Filvaroff,
                                                                             Goddard, A.
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Desnoyers, Luc
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-10
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LENGTH: 915
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APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
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FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
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FILING DATE: 1999-09-08
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APPLICATION NUMBER: US 60/146,222
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APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US99/30095
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, Jennie P.
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: DS 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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Ashkenazi, Avi
Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValAlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePheAlaIleGlyVal 196
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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Filvaroff, Ellen
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Eaton, Dan L.
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Best Local Similarity:
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PRIOR FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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FILING DATE: 1999-12-20
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                           GGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTG
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                                                                                                                                                                                                                                                                                  GETGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACT
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                                                           ValAlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePheAlaIleGlyVal
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               PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30995
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30999
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CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT
FILING DATE: 2000-01-05
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Goddard, A.
Goddwski, Paul J.
Gorimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Botstein, David
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Mather, Jennie P.
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Filvaroff, Ellen
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Eaton, Dan L.
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art, Timothy A.
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Best Local Similarity:
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Pred. No.:
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LENGTH: 915
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APPLICANT: Ashkenazi
APPLICANT: Botstein,
APPLICANT:
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                                                     Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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             Godowski, Paul J.
Grimaldi, Christopher
                                                                                                             Ferrara, Napoleone
Filvaroff, Ellen
Gurney,
                                           Goddard,
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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ORGANISM: Homo
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APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/30095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/30999
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Kljavin, Ivar J.
Mather, Jennie P
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Roy, Margaret Ann
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Conservative:
Mismatches:
Indels:
Gaps:
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CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
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Patent No. 6818449
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TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                   FILE REFERENCE: 10466-14
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                  FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
APPLICATION
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Botsteir
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Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                 Roy, Margaret Ann
Stewart, Timothy A.
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Gerritsen, Mary E.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                   Tumas, Daniel
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                  James
NUMBER: PCT/US99/20594
                                                                                                                                                                                                                                                                                                                                                                             Nicholas F.
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LENGTH: 915
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OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: 1999-12-16
OR APPLICATION NUMBER: PCT/US99/30911
OR FILING DATE: 1999-12-20
OR APPLICATION UMBER: PCT/US99/30999
OR APPLICATION UMBER: PCT/US99/30999
OR FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/20944
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PILING DATE: 1999-12-02
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GlyGlnValAspPheAsnThrLeuLysSerIleGlySerGluProHisGluAspHisVal
                                     GGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTG 474
                                                                                                                                                         LeuArgGluAsnValProArgValIleMetIleValThrAspGlyArgProGlnAspSer
                                                                                                                                                                                          GGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCA
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                                                                          ValAlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePheAlaIleGlyVal 196
                                                                                                                  GTGGGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACC
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APPLICANT:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CHERENUM NOTE: 10466-14
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APPLICANT: Ashkenazi, Av
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OR APPLICATION NUMBER: US 60/145,698
OR FILING DATE: 1999-07-26
OR APPLICATION NUMBER: US 60/146,222
OR FILING DATE: 1999-07-28
OR APPLICATION NUMBER: POT/US99/20594
OR APPLICATION NUMBER: POT/US99/20594
OR FILING DATE: 1999-09-08
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
  APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
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FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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o. 6818746
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Eaton, Dan L.
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Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        James
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
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Patent No. 6828146
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: Ashkenazi, Avi
: Botstein, David
: Desnoyers, Luc
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Gao, Wei-Qiang
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09906618
                                                                           Gerritsen, Mary
                                                                                                      Gerber, Hanspeter
                                                                                                                                                                            Filvaroff, Ellen
                                                                                                                                                                                                                                 Eaton, Dan L.
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Best Local Similarity:
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US-09-906-618-34
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LENGTH: 915
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PRIOR FILING DATE: 2000-02-22
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CURRENT FILING DATE: 2001-07-16
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/21547
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CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCC 123
                                                            GACCTGATGTTCCTGCTGGACAGCTCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
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Mather, Jennie P.
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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
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GENERAL INFORMATTON
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                                                                                                                                                                                                                                           APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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"--ther, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Filvaroff, Ellen
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Roy, Margaret Ann
Stewart, Timothy A.
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Grimaldi, Christopher
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Eaton, Dan L.
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Botstein, David
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APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944

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Best Local Similarity:
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ORGANISM: Homo
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IOR FILING DATE: 1999-11-29
IOR APPLICATION NUMBER: PCT/US99/28313
IOR FILING DATE: 1999-11-30
IOR APPLICATION NUMBER: PCT/US99/28364
IOR FILING DATE: 1999-12-02
IOR APPLICATION NUMBER: PCT/US99/28565
IOR FILING DATE: 1999-12-02
IOR APPLICATION NUMBER: PCT/US99/30095
IOR APPLICATION NUMBER: PCT/US99/3091
IOR FILING DATE: 1999-12-16
IOR FILING DATE: 1999-12-20
IOR APPLICATION NUMBER: PCT/US99/30991
IOR FILING DATE: 1999-12-20
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IOR FILING DATE: 1999-12-20
IOR APPLICATION NUMBER: PCT/US99/30999
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IOR APPLICATION NUMBER: PCT/US99/30999
IOR APPLICATION NUMBER: PCT/US90/00219
IOR FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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Search completed: February 13, 2006, 13:43:34 Job time : 25.7889 secs

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PheLeuValAlaAsnPheSerGlnIleGluThrLeuThrSerValPheGlnLys 234

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-QC/abss/ABSSWEB_spool/US10699035/runat_13022006_062444_25463/app_query.fasta_1
-DB=PIR -QFMT=Eastan -SUPFIX=pp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RESULT 1
A40020
collagen alpha 1(XII) chain precursor – chicken
N;Alternate names: fibrochimerin C:Snories: Gallus callus (Chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Oba
J. Cell Biol. 115, 209-221, 1991
A; Title: The complete primary structure of type XII collagen shows a chimeric molecule
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site
A; Reference number: A40020; MUID: 92011862; PMID: 1918137
A;Accession: A40020
A; Molecule type: mRNA
A;Residues: 1-3124 <yam></yam>
A;Cross-references: UNIPROT:P13944; UNIPARC:UP10000126D2D; GB:D00824; NID:9222810; P1DN
A; Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and
R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Clsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A; Title: Type XII collagen. A large multidomain molecule with partial homology to type
A; Reference number: A34485; MUID:90062079; PMID:2584192
A;Accession: A34485
A; Molecule type: mRNA
A;Residues: 2456-2758; A; 2760-2802; F; 2804-2976; F; 2978-3124 <gor></gor>
A;Accession: B34485
A; Molecule type: protein .
A; Residues: 2772-2792; 2846-2873 < GOR2>
A;Cross-references: UNIPARC:UPI0000173C3F; UNIPARC:UPI0000173C40
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A; Title: Type XII collagen: distinct extracellular matrix component discovered by CUNA
A; Reference number: A28037; MUID:87317590; PMID:3476925
A; Accession: A28037
A:Molecule type: mRNA

A;Molecule type: mRNA, A;Molecule type: mRNA, A;Residues: 2960-2976, 'F',2978-3074,'AG' <GOR3>A;Residues: 2960-2976, 'F',2978-3074,'AG' <GOR3>A;Cross-references: UNIPARC:UPIO0001712F4; EMBL.M17375; NID:g211649; PIDN:AAA48718.1; A;Note: this sequence has been revised in reference A34485

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A; Introns: 2045/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C; Reywords: alternative splicing; cell binding; coiled coil; connective tissue; disule f; 1221/Domain: signal sequence #status predicted coil; connective tissue; disule f; 24-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted coil.
F; 24-114/Domain: IIIA #status predicted coil.
F; 24-114/Domain: IIIA #status predicted coil.
F; 24-114/Domain: IIIA #status predicted coil.
F; 24-115/Domain: IIIA #status predicted coil.
F; 232-425/Domain: fibronectin type III repeat homology complex coil.
F; 332-441/Domain: fibronectin type III repeat homology coil.
F; 347-354/Domain: fibronectin type III repeat homology coil.
F; 347-354/Domain: fibronectin type III repeat homology coil.
F; 348-2495/Domain: fibronectin type III repeat homology coil.
F; 3495-3496/Domain: fibronectin type III repeat homology coil.
F; 3496-3496/Domain: fibronectin type III repeat homology 
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                           F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F;32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site:
F;2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: h)
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Eur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified
A;Reference number: S23814; MUID:92362621; PMID:1323460
A;Accession: S23814
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A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280
A;Cross-references: UNIPARC:UPI0000173C46; EMBL:X67327
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A;Title: The two splice variants of collagen XII share a
A;Reference number: $28811; MUID:93042014; PMID:1420368
A;Accession: $28811
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A;Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
A;Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45
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A;Refidues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517,
A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517,
A;Record of the control of the
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LysAlaAspValValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheVal
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A; Reference number: PH0844; MUID:92231902; PMID:1567409

A; Accession: PH0844

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Molecule: 'BER', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528, 'C', A; Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN: A; Experimental source: keratinocyte

A; Note: The authory terminal source: keratinocyte

A; Note: The authory terminal source: keratinocyte
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A;Molecule type: mRNA
A;Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Cross-references: UNIPARC:UPI000016B3AC; GB:S51236; NID:g262308; PIDN:AAB24637.1; PID
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A;Accession: A30296
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A;Residues: 815-892, 'E', 894-1439 < PAR>
A;Coss-references: UNIPARC: UPI000016A722; GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96
A;Experimental source: Keratinocyte
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A;Accession: I56328; MUID:93107742; PMID:1469284
A;Accession: I56328; MGBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                    A;Molecule type: protein.
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C
A;Note: two reported peptides cannot be reliably located
R;Greenspan, D.S.
R;Greenspan, D.S.
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A;Residues: 1-2944 <CHR>
A;Cross-references: UNIPAROT:Q02388; UNIPARC:UPI000017A138; GB:L02870; NID:g987124; PIDN R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
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C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_chang
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1996; I84686
C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
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A;Reference number: A54849; MUID:94327588; PMID:8051117
                           A;Status: preliminary; translated from GB
A;Molecule type: mRNA
A;Residues: 2395-2871, S', 2873-2944 <RE2>
                                                                                                                                                                              Hum. Mol. Genet. 2, 273-278, 1993
A; Title: The carboxyl-terminal half of type
A; Reference number: 148103; MUID:93271985; I
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A;Status: not compan
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Cross-references: UNIPARC:UPI000016A724; GB:L06862; NID:g388713; PIDN:AAA89196.1;
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A; Cross-references:
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F:231-318/Domain: Fibronectin type III repeat homology <PWALSF;237-413/Domain: fibronectin type III repeat homology <PWALSF;37-413/Domain: fibronectin type III repeat homology <PWALSF;37-413/Domain: fibronectin type III repeat homology <PWALSF;38-593/Domain: fibronectin type III repeat homology <PWALSF;598-683/Domain: fibronectin type III repeat homology <PWALSF;598-683/Domain: fibronectin type III repeat homology <PWALSF;76-6862/Domain: fibronectin type III repeat homology <PWALSF;76-7954-1045/Domain: von Willebrand factor type A repeat homology <PWALSF;71052-1219/Domain: von Willebrand factor type A repeat homology <PWALSF;71052-1219/Domain: von Willebrand factor type A repeat homology <PWALSF;711052-1219/Domain: cell attachment (R-G-D) motif F;1134-1345/Region: cell attachment (R-G-D) motif F;253-2555/Region: cell attachment (R-G-D) motif F;253-2555/Region: cell attachment (R-G-D) motif F;263-2545/Domain: carboxyl-terminal nonhelical #status predicted <PWALSF;786,1109/Binding site: carbohydrate (Asn) (covalent) #status predicted F;2167,2176,2185,2188,2644,2667,2673/Modified site: 4-hydroxypyroline (Pro) #status F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status Fyaff S;2631/Binding site: carbohydrate (Lys) (cova
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A;Title: Dominant dystrophic epidermolysis bullosa: identification A;Reference number: A55255; MUID:94224777; PMID:8170945
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A;Contents: annotation
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A;Note: defects in this gene can result in dominant and recessive
A;Note: there are 118 introns
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217 GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC
                                                                                                                                                                                                                     163 GAGTTTGTGGGGCAGCTGGTTGCCTCCACTGCGCCACCGGGGCC-----CTGCGT
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                                                                                                                                                                                                                                                                                                                             39 IleValPheLeuLeuAspGlySerSerSerIleGlyArgSerAsnPheArgGluValArg
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-GACGTGGATGACCTGCACATCATTGTCCAA-----

609 310 558 =

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270 438 250 378 230 318 210 190

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C;Keywords: alternative splicing; coiled coil; extracellular matrix; F;1-28/Domain: signal sequence #status predicted <SIG>F;1-28/Domain: signal sequence #status predicted <SIG>F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status p F;29-110/Domain: fibronectin type III repeat homology <FN3A>F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1F;352-433/Domain: fibronectin type III repeat homology <FN3B>F;442-525/Domain: fibronectin type III repeat homology <FN3C>F;534-614/Domain: fibronectin type III repeat homology <FN3E>F;623-707/Domain: fibronectin type III repeat homology <FN3E>F;741-823/Domain: fibronectin type III repeat homology <FN3F>F;381-914/Domain: fibronectin type III repeat homology <FN3F>F;322-1009/Domain: fibronectin type III repeat homology <FN3H>F;1040-1205/Domain: fibronectin type III repeat homology <FN3D-F
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C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C;Accession: S31212
R;Waelchli, C:; Trueb, J:; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Bur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31212
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C;Keywords: alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1857 <WAE>
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A;Molecule type: mRNA
A;Residues: 1-1888 <TRU>
A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:g2
A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:g2
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31211
A;Statue: preliminary
A;Molecule type: mRNA
A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793
C;Genetics:
                                                                                                                                                                       submitted to the EMBL Data A; Reference number: S78476 A; Accession: S78476 A; Molecule type: mRNA
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578476
collagen alpha 1(XIV) chain precursor,
collagen alpha 1(XIV) chain precursor,
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision
C;Accession: S78476; S31211
R;Trueb, B.
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                 ValSerTrp---
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A;Gene: Col14A1

C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;

F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;356-320/Domain: fibronectin type III repeat homology <FN3C>
F;352-43J/Domain: fibronectin type III repeat homology <FN3C>
F;352-43J/Domain: fibronectin type III repeat homology <FN3D>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;534-614/Domain: fibronectin type III repeat homology <FN3E>
F;741-82J/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3F>
F;922-1009/Domain: fibronectin type III repeat homology <FN3F>
F;1040-1205/Domain: fibronectin type III re
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                                                                               CTGGCCTGGCCACCCCTGCTGACCGCAGACTCGGGC------
                                                                                                                                                   AlaSerLeuGlyAlaProThrAspLeuValThrSerAspIleThrAlaArgGlyPheArg
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collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Canc J. Biol. Chem. 268, 12177-12184, 1993
A;Accession: S22916
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
A;Cross-references: UNIPARC:UPI0000173C48
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest
                                                                                                 A;Cross-references: UNIPARC:UPI00000006A2; EMBL:X65122; R;Trueb, J.; Trueb, B.
Eur. J. Biochem. 2007, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
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A; Residues: 1472-1660 <APT>
                                                                                                                                                                                                                     A; Reference number: A; Accession: S30085
                                                                                                                                                                                                                                     A; Reference number: S30085
                                                                                                                                                                                                                                                                                                       A; Experimental source: embryo skin A; Note: sequence inconsistent with the nucleotide translation
                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA; protein
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                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: P32018; UNIPARC: UPI0000173C47
                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-1747 <GER>
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A45974; MUID: 93280195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Type XIV collagen is encoded by alternative transcripts with distinct 5'
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A; Residues: 1472-1659
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C;Keywords: alternative splicing; coiled coil; extracellular matrix; F;40-204/Domain: von Willebrand factor type A repeat homology <VWAl>F;436-317/Domain: fibronectin type III repeat homology <FN3A>F;326-409/Domain: fibronectin type III repeat homology <FN3B>F;418-498/Domain: fibronectin type III repeat homology <FN3C>F;418-498/Domain: fibronectin type III repeat homology <FN3D>F;507-591/Domain: fibronectin type III repeat homology <FN3B>F;625-707/Domain: fibronectin type III repeat homology <FN3B>F;716-798/Domain: fibronectin type III repeat homology <FN3F>F;9806-893/Domain: fibronectin type III repeat homology <FN3G>F;9806-893/Domain: fibronectin type III repeat homology <FN3G>F;964-1089/Domain: non-collagenous NC4 #status predicted <NC4>F;1511-1553/Domain: non-collagenous NC4 #status predicted <NC2>F;1554-1659/Domain: triple helical domain COL1 #status predicted <COl
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A; Residues: 1551-1570; 1593-1599; 1639-1667
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A;Title: Cloning of a cDNA for a new member of the class of fibril-associated A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-929 <MEID: A;Rosidues: 1-929 <MEID: A;Cross-references: UNIPROT:091145; UNIPARC:UPI0000126D2: F;155-336/Domain: fibronectin type III repeat homology <
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;155-236/Domain: fibronectin type III repeat homology <3FR>
;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Biol. 168, 503-513, 1995
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A;Molecule type: mRNA
A;Residues: 1-843 <JUS>
A;Cross-references: UNIPROT:Q05707; UNIPARC:UPI00000716A9; GB:M64108; NID:g340081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Just, M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripier, D.; Stein, H.; Schuppan, D. J. Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular A;Reference number: A40970; MUID:91373351; PMID:1716629
A;Accession: A40970
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40970
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                        HisAlaIleThrGlyProProThrGluLeuIleThrSerGluValThrAlaArgSerPhe
                                                                CTCGCGATGCGG-----
                                                                                                                                                                                           AspSerThrHisValTyrAsnValAlaGluPheAspLeuMetHisThrValValGluSer
                                                                                                                                                                                                                                   GCCGAGAAGCACCTGCACTTTGTG---GACGTGGATGACCTGCACATCATTGTCCAA---
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A,Contents: annotation; protein coding region
C,Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, C,Superfamily: human herpesvirus 4 BHLF1 protein
                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P03181; UNIPARC:UP1000000CDC0 R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Nature 310, 207-211, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B Mol. Biol. Med. 1, 21-45, 1983
A;Tille: Sequence analysis of the 17,166 bp EcoRI fragment A;Reference number: A93065; MUID:85035713; PMID:6092825
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Alignment Scores: Pred. No.: 5.42e-07 Length: 493	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-493 <kis> A;Cross-references: UNIFOT:P05099; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; GB:X12 R;Argraves; W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F. Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987 A;Title: Structural features of cartilage matrix protein deduced from cDNA. A;Reference number: A26364 A;Accession: A26364 A;Accession: A26364 A;Molecule type: mRNA A;Residues: 78-493 <arc> A;Cross-references: UNIPARC:UPI000004F1EE; GB:M14792; NID:g211545; PIDN:AAA48695.1; PID C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repeat homology <vwa1> F;37-204/Domain: von Willebrand factor type A repeat homology <vwa2> F;270-434/Domain: von Willebrand factor type A repeat homology <vwa2></vwa2></vwa2></vwa1></arc></kis>	RESULT 9 A33809 A33809 cartilage matrix protein precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004 C;Accession: A33809; A26364 R;Kiss, I.; Deak, F; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Arg J. Biol. Chem. 264, 8126-8134, 1989 J. Biol. Chem. 264, 8126-8134, 1989 A;Title: Structure of the gene for cartilage matrix protein, a modular protein of the egrins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor. A;Reference number: A33809; MUID:89255246; PMID:2542265 A;Accession: A33809	

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US-10-699-035A-5 (1-1254) x JQ0405 (1-1106)	Alignment Scores: Pred. No.: Core: Score: Score: Percent Similarity: Best Local Similarity: Conservative: Conserva	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1106 <shi> A; Residues: 1-1106 <shi> A; Cross-references: UNIPARC:UPI0000177394; EMBL:X15867 A; Cross-references: UNIPARC:UPI0000177394; EMBL:X15867 A; Mote: this reading frame extends between two stop codons and does not begin with a sta A; Mote: the gene encoding this protein overlaps uvrA gene C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;</shi></shi>	C;Species: Micrococcus luteus, Micrococcus lysodeikticus C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000 C;Accession: JQ0405 R;Shiota, S.; Nakayama, H. Mol. Gen. Genet. 217, 332-340, 1989 A;Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: identification of A;Feference number: S04781; MUID:89364717; PMID:2549377	sne	Qy 535 TCAGCCGCTGCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGAT 588	QY 475 AAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACCTTCCTGGAGCTG 534	Qy 415 CTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCCATGCAGGAGCTC 474	Qy 355 TATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTG 414	Oy 295 GATGCGGTGCGTGCTTCTGCCCAGGGGATGGGTGACACCCACACTGGCCTGGTC 354 :::	Qy 235 GGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTTGGGGTGAGGCTGGCCCAG 294	Oy 175 CAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTG 234 :::	Qy 115 CTGGACAGCTCAGCGACGTCTCTCACTACGAGTTCTCCCGGGTTCGGGGAGTTTGTGGGG 174	Oy 73 GGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTG 114	2 Gaps: 5A-5 (1-1254) x A33809 (1-493)	Score: 248.50 Matches: 66 Percent Similarity: 49.4% Conservative: 22 Best Local Similarity: 37.1% Mismatches: 83 Ouery Match: 10.4% Indels: 7
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A;Molecule type: mRNA
A;Residues: 1-500 <ASZ>
A;Cross-references: UNIPROT:P51942; UNIPARC:UPI0000029480; EMBL:U35035
A;Geneet.cs:
A;Gene: CMP
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-500/Product: cartilage matrix protein #status predicted <MAT>
F;43-210/Domain: von Willebrand factor type A repeat homology <VWA1>
F;231-266/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                       cartilage matrix protein precursor - mouse (;Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 (;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 (;Accession: S66522 R;Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z. R;Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z. Eur. J. Biochem. 236, 970-977, 1996
                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of
A;Reference number: S66522; MUID:96270751; PMID:8665920
A;Accession: S66522
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A;Cross-references: UNIPROT:P03181; UNIPARC:UPI000000CDC0 R;Baer, R.; Bankler, A.T.; Biggin, M.D.; Deininger, P.L.; Farre Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr A;Reference number: A03794; MUID:84270667; PMID:6087149
                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI A;Reference number: A93065; MUID:85035713; PMID:6A;Accession: A03742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 (;Accession: A03742
                                                                                                                                                                                                                    A;Contents: annotation; protein coding region C;Comment: The sequence contains four perfect repeats C;Superfamily: human herpesvirus 4 BHLF1 protein
                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-660 < BAN>
US-10-699-035A-5 (1-1254) x QQBE3 (1-660)
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A;Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
C;Superfamily: polymorphic epithelial mucin
C;Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorphis
F;1-1344/Product: mucin 1 precursor, splice form A #status predicted <PREA>
F;1-62/Region: mucin 1 amino-terminal non-repetitive
F;1-62/Region: mucin 1 amino-terminal precursor splice form B #status predicted <SIGB>
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <PREB>
F;1-19,29-1344/Product: mucin 1 precursor, epithelial tumor antigen splice form F;138-1017/Region: 20-residue repeate (SIGRAPAHGYTSAPDTRPAP)
F;318-1017/Region: 20-residue repeates (SIGRAPAHGYTSAPDTRPAP)
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A;Title: A novel core protein as well as polymorphic epithelial mucin carry peanut agglu A;Reference number: JX0235; MUID:93123189; PMID:1478919
A;Accession: PX0066...
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A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Residues: In-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Rote: GenBank entry HUMPANNU contains four fewer copies of the tandemly repeated seque R;Wreschner, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J.
Bucchem. 189, 463-473, 1990
A;Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may general A;Reference number: S10571; MUID:90276413; PMID:2351132
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C;Comment: Serine and threonine residues in the tandem repeat domain are extensively g1: C;Comment: For an alternative splice form without a tandem repeat domain, see PIR:S4814.
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A;Restdues: 1-19,29-155,'p',157-175,'p',177-182,'A',184-212,1033-1037,'A',1039-1344 <WR2
A;Restdues: 1-19,29-155,'p',157-175,'p',177-182,'A',184-212,1033-1037,'A',1039-1344 <WR2
A;RCOOSS-TEFGETENCES: UNIPARC:UPI000016B0A6; EMBL:X52229; NID:g37053; PIDN:CAA36478.1; PID
R;Abe, M.; Siddiqui, J.; Kufe, D.
Biochem. Biophys. Res. Commun. 165, 644-649, 1989
Biochem. Biophys. Res. Commun. 165, 644-649, 1989
A;Title: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated
A;Reference number: A36735; MUID:90088473; PMID:2597151
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                                                                             Best Local Similarity:
                                                                                                                                                   Percent Similarity:
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;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344 <WRE>
;Cross-references: UNIPARC:UPI0000174569; EMBL:X52229; NID:g37053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1143-1344/Region: mucin 1 carboxyl-terminal non-repetitive
.1245-1272/Domain: transmembrane #status predicted <TRM>
.1046-1064.1118.1144.1222/Binding site: carbohydrate (Asn) (covalent) #status predicted
.1046.1064 tills.1144.1222/Binding site: carbohydrate (Asn) (covalent) #status predicted
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1.51e-06
240.00
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28.3%
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Matches:
Conservative:
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                     GTTCCTTGGCATAGACCAGCCCAGGCCAGTGTGGGGTGTCACCCATGCGCTGGGCAGAAG
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TGTGGGTGTCACCCATGCGCTGGGCAGAAG 308	GTTCCTTGGCATAGACCAGCGCCAGGCCAGTGTGGGTGT	/ 367	Ş
aHisGlyValThrSer 889	ProAlaProGlySerThrAlaProProAlaHisGlyVal-	875	뫄
TGCTT	TCACCCACACCAGCACTTTGGGCACCCCTGGCCGGCAC	427	8
aProAspThrArg 874	ThrSerAla	3 860	ఠ
1	-C	475	S
ThrArgProAlaProGlySer 859	SerAlaProAspThrArgProAlaProGlySer	849	뫄
ACAATGAACACGGTGACGCCCAGGTCCT 476	ACAGCTCCAGGAAGTTGCCTCGGCCGGTGCTGACAATGA	535	Ş
oProAlaHisGlyValThr 848	AspThrArgProAlaProGlySerThrAlaProProAlaHisGlyV	832	Дb
TTCTCGGCAGGGGCTGAGGCAGCGGCTG 536	CATCCACGTCCACAAAGTGCAGGTGCTTCTCGGCAGGGGCTGAGGCAGCGGCTG	, 589	ð
erAla	AspThrArgProAlaProGlySerThrAlaProProAlaHisGlyValThrS	812	ם
ATGATGTGCAGGT 590	TCGCGAGAATGGAGCCCCTCAGCTCTTGGACAATGATGT	634	Ş
oProAlaHisGlyValThrSerAlaPro 811	ProGlySerThrAlaProProAlaHisGlyValThrSerAl	797	뫄
TCCGTGGCATGGAGCTGCTGCGGCCGCA 635	GCCAGGCCAGGCGAAGCCGCTGGACGTGATCTCCGTGG	694	Š
	ThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAla	780	дd
TAGCCCGAGTCTGCGGTCAGCAGGGGTG 695	TGGGCACCAGCTCCAGCACATAGTAGCCCG	745	δ
aProAspThrArgProAlaProGlySer 779		763	Дb
TGGCGTCTTGCAGCCCCGGCTGGGCGC 746	AGT	, 805	Š
xArgProAlaProGlySerThrAlaPro 762	AlaProAspThrArgProAlaProGlySerThrAlaPro	750	Db
TAGTCCGTGTCCGGGTCGAGGCCGGCCC 806	ິດ	, 865	γQ
aProProAlaHisGlyValThrSer 749	ThrArgProAlaProGlySerThrAlaProProAlaHisGlyValThrSer	733	ర్జ
ACCCGCAGGATCTGGGGCCTCAGGAGGC 866	GCTCTGGCCCGGGCCTCCTGGCCGCGTGCGCACCCGCA	, 925	ð
:: rSerAlaProAsp 732	GlySerThrAlaProProAlaHisGlyValThrSerAlaProAsp	718	닭
CGCGGCCGGGCGTGGGAGATGACGATGC 926	GGGCCCAACTCACGCGGAGGCTGCGCGGCC	, 976	Ş.
rSerAlaProAspThrArgProAlaPro 717	GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro	698	뮍
GCGCCGCCTGAGCCCAGCGCTG 977	GCCCGAACTGCACGTGGTAGCCGAGCG	, 1024	Š
rSerAlaProAspThrArgProAlaPro 697	O O	678	ద
- 1		1054	δ
 ProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 677	 	658	da da
TTGCGGCCCGCGGGCACCT 1055		, 1093	Ş
::: rAlaProAspThrArgProAlaPro 657	ProProAlaHisGlyValThrSerAlaProAspThrArgProAla	642	Дb
GTCACCAGGTAGGCGGTGCCCGGCGA 1094	TCTCGCGGCCCGAGCGGAAGGCGGCGGTCACGGTCACCA	, 1153	δ
gProAlaProGlySerThrAla 641	AlaHisGlyValThrSerAlaProAspThrArgProAlaProGlySerThrAla	624	DЬ
GGCGTGCAGGCCTTGGCGGACAGCGCGC 1154	GCACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	, 1213	γQ
gProAlaProGlySerThrAlaProPro 623	 AlaHisGlyValThrSerAlaProAspThrArgProAlaProGlySer	604	망
CCGGGGTCGGGGCGCGGG 1214	GCTCACGGCTGGCGGTCC	1249	ઇ ∴
	A-5 (1-1254) x A35175 (1-1344)	-10-699-035	ŭ
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Query
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                                                                                                                                                                                                                                                                             C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand C;Keywords: glycoprotein; homotrimer
F;1-22/Domain: signal sequence #status predicted <SIG>
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A;Cross:references: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: UNIPARC:UPI000016A6EB; GB:M55683;
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A;Title: Structure and chromosomal location of the human gene
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                                                       Percent Similarity:
Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                   ;227-262/Domain: EGF homology <EGF>
;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
;76,344/Binding site: carbobydrate (Asn) (covalent) #status predicted
;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                               No.:
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50.3%
35.0%
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    CCTGGGCAGCCTCACCCGAGCTGTGCTGGCCGAAGG

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C; Genetics:
A; Introns: 30/1
C; Superfamily:
                                                         A;Title: The carboxyl terminus of the chicken alpha3 chain A;Reference number: A32674; MUID:90062147; PMID:2584214 A;Accession: A32674 A;MCID:90062147; PMID:2584214 A;Residues: 2151-2199;2792-3137 <B02> A;Cross-reference
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A37797
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A;Note: the authors translated the codon TTC for residue
                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 224-2871 <BON>
                                                                                                                                                                                                                                                                                                    A;Title: Structural and functional features of the alpha3 A;Reference number: A34270; MUID:90212613; PMID:2322559
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                     236/1;
     437/1; 638/1; 838/1
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collagen alpha 3(VI) chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A37797; A34270; A32674
C;Accession: A37797; A34270; A32674
C;Cell Biol. 111, 2197-2205, 1990
A;Title: Multiple forms of chicken alpha3(VI) collagen chain generated by alternat A;Reference number: A37797; MUID:91035630; PMID:1977751
A;Accession: A37797
A;Molecule type: mRNA
A;Residues: 1-53;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A;Cross-references: UNIPROT:P15989; UNIPARC:UPI0000173C31; UNIPARC:UPI0000173C32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Bonaldo, P.; Russo, V.; Bucciotti, F.; Doliana, R.; Colombatti, Biochemistry 29, 1245-1254, 1990
A;Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI0000173C3A;
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LysLysPheIleSerGlnIleValAspThrLeuAspValSerAspLysLeuAlaGlnVal 314
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C;Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracel F;1-25/Domain: signal sequence #status predicted <SIG>F;26-3137/Product: collagen alpha 3(VI) Chain #status predicted <MAT>F;26-3137/Product: collagen alpha 3(VI) Chain #status predicted <MAT>F;26-3042/Domain: con-collagenous #status predicted <NNC>F;26-2042/Domain: von Willebrand factor type A repeat homology <VW002>F;402-607/Domain: von Willebrand factor type A repeat homology <VW004>F;36-202/Domain: von Willebrand factor type A repeat homology <VW005>F;402-807/Domain: von Willebrand factor type A repeat homology <VW005>F;403-197/Domain: von Willebrand factor type A repeat homology <VW006>F;1033-1197/Domain: von Willebrand factor type A repeat homology <VW007>F;139-1804/Domain: von Willebrand factor type A repeat homology <VW007>F;1439-1604/Domain: von Willebrand factor type A repeat homology <VW009>F;1639-1804/Domain: von Willebrand factor type A repeat homology <VW009>F;1639-1804/Domain: von Willebrand factor type A repeat homology <VW009>F;1639-21804/Domain: von Willebrand factor type A repeat homology <VW10>F;2043-2378/Domain: collagenous #status predicted <COL>F;2045-2047/Region: cell attachment (R-G-D) motif F;2153-2153/Region: cell attachment (R-G-D) motif F;2379-3137/Domain: von Willebrand factor type A repeat homology <VW11>F;263-2806/Domain: von Willebrand factor type A repeat homology <VW12>F;263-2806/Domain: on illebrand factor type A repeat homology <VW12>F;263-2806/Domain: on willebrand factor type A repeat homology <VW12>F;263-280
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                                                      SerSerValLeuLysSerAlaHisValAsnMetIleAlaValGlyValGlnAspAlaVal 180
                                                                                                                                                                                                                                CTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCCGG-----CCAGGG 402
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   TTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTG---CACTTTGTG
                                                                                                             ATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAAC
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Search completed: February 13, 2006, 13:41:49 Job time: 78.062 secs

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Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006_062441_25416/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10699035_@CGN 1_1_580_@runat 13022006_062441_25416 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -NAGAPOP=10 -NGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Q4nra5 anaeromyxob	Q9q5k9 cercopithec	_	Q4nqb4 anaeromyxob	Q4nuu3 anaeromyxob		Q4nqy7 anaeromyxob		Q4nra5 anaeromyxob	Q4nx38 anaeromyxob	Q6nti5 brachydanio	homo	Q05707 homo sapien	Q4sh63 tetraodon n		Q90za0 gallus gall	Q63870 mus musculu	Q4sxe3 tetraodon n	Q7yrk8 canis famil	P32018 gallus gall	O97566 canis famil	homo	Q8ivx1 homo sapien	homo	homo	homo	Q4vxq4 homo sapien	Q4rp12 tetraodon n	Q4rxn8 tetraodon n

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InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
PRINTS; PR00453; VWFDOMAIN.
SMART; SM0050; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWBA; 1.
PROSITE; PS50234; VWBA; 1.
SEQUENCE 445 AA; 46804 MW; DS
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                                               GCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATC
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                                    AlaAlaSerAlaProAlaGluLysHisLeuHisPheValAspValAspAspLeuHisTle
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                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna Muroidea; Muridae; Murinae; Mus. NCBI TaxID=10090; [1]
 TISSUE=Colon, and Mammary tumor metastatized to lung. MEDLINE=22388257; PubMed=12477932; I
                                     NUCLEOTIDE SEQUENCE.
STRAIN=Czech II, and
                                                                                                                          Mus musculus (Mouse)
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                                     FVB/N;
                                                                                                                                                                                                                                                                                                                            1251
                                                                                                                                                                                                                                                                                                      445
  Tumor arose spot DOI=10.1073/pnas
   spontaneously;
pnas.242603899;
                                                                                                 Sciurognathi;
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360

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340

300

777 260 837 280 897

903

1176

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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsteh F.R.
RA Liatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-1-----
N [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RC STRAIN=CS7BL/6J; TISSUE=Ovary and uterus;

RM MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RM MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Mawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Airawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Barakov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Hornstein M.J., Bult C., Righald M., Rodriguez I., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sazaki H., Sato K., Schoenbach C., Seya T., Shbata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Havsenki Z., V., Scholada K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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60,770 ful
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                        STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDN
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    full-length
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A Adachi J., Aizawa K., Akimura T., Brakawa T., Bono H., Carninci P.,

A Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

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A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

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A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

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MEDLINE=20530913; PLDMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

KORNO H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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GO; GO:0005615;
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EMBL; AK077240; BAC36703.1;
EMBL; BC036166; AAH36166.1;
HSSP; P18614; 1MHP.
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Director MGC Project;
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PF00092; VWA; 1.
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AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGGCAGCTG
                                                                                                                   GGCGCGGAGCGCGGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGAC
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||| |||:::::: |||||::: ||| |||:::||| Arg--AlaProGlnSerMetArgProGluAlaGlyProArgGluPro
                            ceccaceccceaeccccececcccaacccceeeaacceccaecce
                                                      GGCTACTATGTGCTGGAGCTGGTGCCCAGCGCCCAGCCGGGGGCTGCAAGACGCCAGCAG
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OS23K3 MOUSE PRELIMINARY; PRT; 415 AA.

OS23K3,

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Matches:
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Q8COQ7;
                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length (library, clone:4932416A11 product:VON WILLEBRAND FACTOR PROTEIN homolog.
                          Name=Vwa1; Synonyms=4932416A11Rik; Mus musculus (Mouse).
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    RC STRAINE-C79BL/6J; TISSUB=Testis;

RC MEDLINE-2108566; PubMed=11217851; DOI=10.1038/35055500;

RA MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Shibata K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

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RA Alzawa K., Okazaki Y., Gojobori T., Bonoo H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Hyoshight H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Havashizaki Y.,
                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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"RIKEN integrated sequence analysis (Risa) system-384-format

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STRAIN=C57BL/6J; TISSUE=Testis; Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carnii Adachi J., Alzawa K., Kahimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hirozane W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane Mori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
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NUCLEOTIDE
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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prepare full-length cDNA libraries for rapid discovery of
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium, the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Muroidea; Muridae; Murinae;
NCBI TaxID=10090;
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InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; Kn3; 2.
Pfam; PF00041; Kn3; 2.
Pfam; PF000453; VWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; VWFA; 1.
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EMBL; AK030019; BAC26739.1; -; mRNA.

HSSP; P18614; 1MHP.
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MGI:2179729; 4932416A11Rik.
MGI:2179729; Vwal.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
75-OCT-2004 (TrEMBLrel. 28, Created)
TISSUE=Kidney;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Diatthenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Josares M.B., Toshiyaki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
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Rattus norvegicus (Rat)
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Submitted (SEP-2004) to the EMB;
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EMBL; BC081983; AAH81983.1; -; |
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SWART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44832 MW;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F., Diattchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Homo papiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003543; AAH03543.2; -; mRNA.
InterPro; IPR003961; FN III.
Ffam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS0065; FN3; 1.
PROSITE; PS05053; FN3; 2.
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SEQÜENCE 281 AA; 29628 MW; 350CCE4590791BD4 CRC64;
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RESULT 7
Q9H6J5 HUMAN PRELIMINARY;
ID Q9H6J5 HUMAN PRELIMINARY;
AC Q9H6J5;
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Ensembl; ENSG00000179403; Homo s
InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS50853; FN3; 2.
                                                                                                                                                                                                                                                                                                  Watanabe K., Kumagai A., Itakura S., Yamazaki Suzuki Y., Obayashi M., Nishi T., Shibahara T. Nakamura Y., Isogai T., Sugano S.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ EMBL; AK02568; BAB15264.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein FLJ22215.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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PS50853; FN3; 2.
233 AA; 24473
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ibahara T., Ta
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RESULT 8

Q8VDV9 MOUSE
ID Q8VDV9;
AC
Q8VDV9;
AC
Q8VDV9;
AC
Q8VDV9;
AC
Q8VDV9;
AC
Q8VDV9;
DT
O1-MAR-2002 (TrEMBLrel. 20
DT
O1-MAR-2004 (TrEMBLrel. 20
DT
O2 (Mammalia; Eutheria; Euarch
OC
MAMMAlia; Eutheria; Eucheria
RA
Altschul S.F.; Zebbreg B.,
RA
OLICHOTIDE SEQUENCE.
RA
Altschul S.F.; Zebbreg B.,
RA
Alts
                              TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

RC TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

RX MEDLINE-22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Blackerin M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bar S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Warny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mhiting M., Maran J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generstin and initial manivois of Force than 15 0.00 full length human
"Generstin and initial manivois of Force than 15 0.00 full length human
"Generstin and initial manivois of Force than 15 0.00 full length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Vwa1; Synonyms=4932416AllRik; Mus musculus (Mouse).
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RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., RA Jaillon O., Aury J.M., Brunet C., Ozouf-Costaz C., Bernot A., RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard C., buprat S., Brottier P., Coulain J., De Berardinis V., RA Griaud C., buprat S., Brottier P., Coutanceau J.P., Gouzy J., RA Criaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., RA Calis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Rollis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Rollis M., Guigo R., Scay M.C., Kahn D., Robinson-Rechavi M., Ra Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";

Nature 431:946-957 (2004).
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13-SEP-2005
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Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14859, whole genome shotgun sequence.
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                                                                                                      ThrGlnSerSerLeuGlnGlySerLeuArgAsnIleLysProLeuArgGlyAspThrAsn
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                                                                                         COCA1_CHICK STANDARD; PRT; 3124 AA. P13944; Q04509; 01-JAN-1990 (Rel. 13, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update Collagen alpha 1(XII) chain precursor (Fibr
    Archosauria; Aves; Gallus.
                                                              Name=COL12A1;
Gallus gallus (Chicken)
                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                          CHICK
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|AspileAspAspMetSerileIleThrAspAspLeuArgAspAlaileIle
                        Neognathae;
                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::
                                                                                                                                                                                                                                                                                                         419
                        Galliformes;
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                                                                                                           update)
(Fibrochimerin)
                          Phasianidae;
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                          Phasianinae;
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NCBI_TaxID=9031;

type-III al (TSPN)

domains domain.

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MEDLINE=95370352; PubMed=7642694; DOI=10.1083/jcb.130.4.1005;
KOch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.
"Large and small splice variants of collagen XII: differential
expression and ligand binding.";
J. Cell Biol. 130:1005-1014(1995).
-i- FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COL1 domain could be associated with the
surface of the fibrils, and the COL2 and NC3 domains may be
localized in the perifibrilar matrix.
-i- SUBUNIT: Trimer of identical chains each containing 190 kDa of
nontriple-helical sequences.
-i- ALTERNATIVE PRODCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Embryo;

MEDLINE-93042014; PubMed=1420368; DOI=10.1016/0167-4781(92)90145-P;

Trueb J., Trueb B.;

"The two splice variants of collagen XII share a common 5' end.";

Biochim. Biophys. Acta 1171:97-98(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE MEDLINE=87317590; Po
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J. Biol. Chem. 264:19772-19778(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 1-1283 (ISOFORM SHORT), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Type XII collagen: distinct extracellular matrix component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon M.K.,
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                                                                                                                    each
PTM:
                                                                                                                                                                       ligaments, perichondrium, and periosteum, all dense tissues containing type I collagen.

DOMAIN: This sequence defines five distinct domains, helical domains (COL) and COL2) and three nontriple-l domains (NC1, NC2, and NC3).

PTM: The triple-helical tail is stabilized by disulfi
                                                                                                                                                                                                                                                                                                                  Name=Short;
IsoId=P13944-2; Sequence=VSP 001148;
TISSUE SPECIFICITY: Type XII collagen is present in tendons,
TISSUE specification, and periosteum, all dense connect:
                            unit
PTM:
(By E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2; Comment=The final tissue form of collagen II may contain homotrimers of either isoform Long or isoform Short or any combination of isoform Long and isoform Short. Only isoform Long is a proteoglycan. Isoform Long has more restricted expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P13944-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning.";
atl. Acad. Sci. U.S.A.
                            : Prolines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in some or all of the chains. O-glycosylated; glycosaminoglycan of chondroitin-sulfate tysimilarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     embryonic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Gerecke D.R., Olsen B.R.;
Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ဝှင့
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fibril-associated collagens with
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in molecule with partial homology
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                                                                                                                                                                                                                                         nontriple-helical
                                                                                                                                                                                disulfide
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EMBL; D00824; BAA00701.1; -; m

EMBL; X61024; CAA43358.1; -; m

EMBL; M17375; AAA48718.1; -; m

EMBL; J05137; AAA48635.1; -; m

EMBL; X67327; CAA47744.1; -; m

PTR; A40020; A40020.
                                                                                                                                                                                                        Hydroxylation; 1
SIGNAL 1
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PROSITE; PS50234; VWFA; 4.
Alternative splicing; Cell adhesion; Collagen;
Direct protein sequencing; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 17. Pfam; PF00092; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             P56199;
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IPR003961; FN_III.
IPR003129; Laminin_G_TSP_N.
IPR002035; VWF_A.
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Arg/Lys-rich (basic).
N-linked (GlcNAc. . .
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Nonhelical region (NC3)
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LysAlaAspValValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheVal
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                      GCGATGCGGCCGCAGCAGCTCCATGCC-----
                                                                                               ThrValGluAspPheAspAlaPheGlnArgIleSerPheGluLeuThrGlnSerValCys
                                                                                                                                 TTTGTG----GACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGGCTCCATTCTC
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S (in Ref. 4).
S E (in Ref. 2).
A (in Ref. 2).
F (in Ref. 2).
F (in Ref. 2).
A G (in Ref. 3).
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Collagen, type XII, alpha 1.
Name=COLL2A1; OFFNames=RP1-23!
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Euarchonto
Submitted (MAY-2005) to the E
EMBL; AL1354664; CAH71309.1; -
EMBL; AL080250; CAI19897.1; -
EMBL; AL096771; CAI19907.1; -
EMBL; AL096771; CAH71309.1; J
EMBL; AL096771; CAH71309.1; J
EMBL; AL056764; CAI11897.1; J
EMBL; AL080250; CAI19907.1; J
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Collagen; Extracellular matrix;
SEQUENCE 2884 AA: 315077
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EMBL; RING90000111799; Homo sapiens.
GO; GO:0005737; C:cyttplasm; IEA.
GO; GO:000578; C:extracellular matrix (sensu Metazoa);
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
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13-SEP-2005 (TrEMBLrel. 31, Last annotati
Collagen, type XII, alpha 1.
Name=COLL2A; ORFNames=RP1-238D15.1-001;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ EMBL; AL354664; CAH71310.1; -; Genomic_DNA. EMBL; AL080250; CAI19898.1; -; Genomic_DNA.
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Eukaryota; Metazoa; C
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GO; GO:0005198; F:structural molecule activity; IE.
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MEDLINE-97288521; PubMed=9143499; DOI=10.1006/geno.1997.4638; Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R., Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.; "Complete primary structure of two splice variants of collagen and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX) collagen (COL19A1) to human
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                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                         (ISOFORMS LONG
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GO; GO:0005595; C:collagen type XII; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR00360; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR00395; WF A.
Pfam; PF01391; Collagen;
Pfam; PF00041; fn3; 18.
Pfam; PF00041; fn3; 18.
Pfam; PF00043; VWFADOMAIN.
PROSITE; PS00853; FN3; 18.
PROSITE; PS00853; FN3; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 41:236-242(1997).

-!- FUNCTION: Type XII collagen interacts with type I collagen containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).

-!- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences.

-!- ALTERNATIVE PRODUCTS:

Comment=The final tissue form of collagen XII may contain homotrimers of either isoform Long or isoform Short or any combination of isoform Long and isoform Short;
                                                                                                                                    Hydroxylation;
SIGNAL 1
CHAIN 25
 DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                Alternative splicing; Cell adhesion; Collagen;
Direct protein sequencing; Extracellular matrix; Glycoprotein;
Hydroxylation; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome
                                                                                                                                                                                                                                                                                                                                                                                              HGNC; HGNC:2188; COL12A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unit (G-X-Y) are hydroxylated in some or all of the chansimilarity).

PTM: O-glycosylation of isoform Long; glycosaminoglycan chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collagens winterrupted helices (PACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=099715-2; Sequence=VSP 001149;
TISSUE SPECIFICITY: Found in collagen I-containing tissues: both isoform Short and isoform Long appear in amnion, chorion, skeletamuscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the short isoform is found in lung, placenta, kidney and a squamous cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: The triple-helical tail is stabilized each end (By similarity).

PTM: Prolines at the third position of the unit (G-X-Y) are hydroxylated in some or al
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U73779; AAD40483.1;
P18614; 1MHP.
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                                                                                                                     Collagen alpha 1(XII) chain. Fibronectin type-III 1.
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                                   CGGGTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTG
                LysValArgAlaPheLeuGluValLeuValLysSerPheGluIleSerProAsnArgVal
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                                                CTGGGCTCAGCCGCGCGCTCCGCTACCACGTGCAGTTCGGGCCGCTGCGGGGCGGGGAG
                                                                                              ArgAspLeuArgValSerAspProThrThrSerThrMetLysLeuSerTrpSerGlyAla
                                                                                                                                            GAGCGCATCGTCATCTCCCACGCCCGGCCGCGCAGCCTCCGCGTGAGTTGGGCCCCAGCG
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RESULT 14
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Nicaud S., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Anthouard C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Rindbad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincher P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                    PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0453; VWFADOMAIN.

SMART; SM00060; FN3; 11.

SMART; SM00327; VWA; 3.

PROSITE; PS50853; FN3; 12.

PROSITE; PS50234; VWFA; 3.

Collagen; Extracellular matrix; SI

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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 14 SCAF14645, whole genome shotgun seque
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Eukaryota; Metazoa; Chordata; Craniatta; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, CAAE01014645; CAG01460.1; -; Genomic_DNA
InterPro; IPR003961; FN_III
InterPro; IPR003962; FnIII subd.
InterPro; IPR003035; VWF_A.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCA1 MOUSE STANDARD; PI
Q60847; P70322;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last seque
10-MAY-2005 (Rel. 47, Last annot
Collagen alpha 1(XII) chain pres
                                                                                                                                                                                                                                                                                                                        "Structural variation of type XII collagen at its carboxyl-terminal NC1 domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274:2203-22059(1999).
-!- FUNCTION: Type XII collagen interacts with type I collagen containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).
-!- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99348349; PubMed=10419532; DOI=10.1074/jbc.274.31.22053; Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R Olsen B.R., Nishimura I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice
collagen XII and their tissue-specific expressic
development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniat;
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Coll2al;
Mus musculus (Mouse)
                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND XIIB-2).
STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL NUCLEOTIDE SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J, and Swiss Webster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XIIB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE, AND ALTERNATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
IsoId=Q60847-4; Sequence=VSP_001150, VSP_001151, VSP_001152; TISSUE SPECIFICITY: Highest expression in tendons, perichondrium, skin, cornea, sclera, blood vessels, and periosteum.

DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are predominant a early stages (ED7 and 11); at later stages of development (ED15 and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice variant continues to be expressed in several tissues, even after birth.
                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=4;
Comment=The final tissue form of collagen XII may contain
homotrimers or any combination of the various isoforms;
                                                                                                                                                                                             Name=XIIA-2; Synonyms=ER#K;
IsoId=Q60847-2; Sequence=VSP_001151,
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                                                                                                                                                         IsoId=Q60847-3; Sequence=VSP_001150;
                                                                                                                                                                                                                                      IsoId=Q60847-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCCGCGC 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCGCCGCCTTCCGCTCGGGCCGCGAGAGCCGCCGCTGTCCGCCAAGGCCTGCACGCCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
chain precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skin;
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Pfam; PF00092; VWA; Pfan; PFam; PF00092; VWA; Pfam; PF00092; VWFADOWAIN.

SWART; SW00060; FN3; 18.

SWART; SW00210; TSPN; 1.

SWART; SW00327; VWA; 4.

PROSITE; PS50853; FN3; 18.

PROSITE; PS50234; VWFA; 4.

Alternative splicing; Cell adhesion; Collagen; Extracellular matrix; PR05176; PS50234; VWFA; 4.

Alternative splicing; Cell, adhesion; Collagen; Extracellular matrix; PR05176; PS50234; VWFA; 4.

Alternative splicing; Cell, adhesion; Collagen; Extracellular matrix; PR05176; PS50234; VWFA; 4.
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EMBL; U57095;
HSSP; P18614;
                           DOMAIN
DO
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InterPro; IPR008160; Collagen.
InterPro; IPR003129; FN III.
InterPro; IPR003129; Laminin_G_TSP_N.
InterPro; IPR002035; VWF_A.
Pfam; PF01391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWA; 4.
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similarity)
PTM: O-glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. There are no restrictions as long as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages of embryonic development (ED15 and ED17).

PTM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).

PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENSMUSG00000032332; Mus musculus
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                             1MHP.
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AAB07047.1;
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               GluPheAsnArgValGluAspIleIleLysAlaIleAsnThrPheProTyrArgGlyGly
                                                                        argValGlnIleSerLeuValGlnTyrSerArgAspProHisThrGluPheThrLeuLys
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                                             TTCTCCCGGGTTCGGGAGTTTGTGGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGG
                                                                                                     GCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGC
                                                                                                                                  PheValLysValArgAlaPheLeuGluValLeuAlaLysSerPheGluIleSerProAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              844 CTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATCCTGCGGGTGCGCACGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           685 AlaSerSerThrSerValValLeuAsnSerLeuArgProGluThrLeuTyrLeuValAsn 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 ValLysAspAlaValArgSerGluLeuGluAlaIleAlaSerProProAlaGluThrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 CCTGTGGGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGC
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Q923K3_MOUSE
Q8C0Q7_MOUSE
Q642A6_RAT
Q81VXI HUMAN
Q4VXO5 HUMAN
Q6P159 HUMAN
Q4VXO4 HUMAN
Q4VXO4 HUMAN
Q1003 HUMAN
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MATN2 HUMAN
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Q4TOK3 TETNG
Q5R9N1 PONPY
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COEA1 MOUSE
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Q4SH63 TETNG
Q5VYK2 HUMAN
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CCEA1_CHICK
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Q5vyk2
Q99715
Q997k1
           Q6p3n7
Q4rxn8
                          Q4t0k3
Q5r9n1
                                                                  Q6pi59
Q4vxq4
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Q8c0q7
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Scoring table: Sequence: Title: Perfect score:

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Q80vn5 mus musculu	Q4rp14 tetraodon n	Q4s2x7 tetraodon n	Q7syt5 xenopus lae		008746 mus musculu	Q569v0 mus musculu	Q5njj2 brachydanio	Q4g0w3 homo sapien	-	Q6pyx2 brachydanio		P05099 gallus gall	Q60847 mus musculu	

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RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsich F.,
RA Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S.A., Northyn M. Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rodrigues S., Sanchez A.,
RA Rodrigues S., Sanchez A.,
RA Rodrigues S., Sanchez A.,
RA Rodrigues A. C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodrigues A. C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodrigues A. C., Grimwood 
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Q6PCBO;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Von Willebrand factor A domain-related protein, isoform 1 (WARP).
Name=WARP; ORFNames=RP4-758J18.11-001;
EMBL; BC059409; AAH59409.1; -; mRNA.
EMBL; AL391244; CA122657.1; -; Genomic
Ensembl; ENSG00000119403; Homo sapiens.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
Pfam; PF00041; fn3; 2.
Pfam; PF000992; VWA; 1.
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Submitted (OCT-2003)
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TISSUE=Placenta;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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SMART; S
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Von Willebrand factor A domain-related protein (Mus musculus 11 days
pregnant adult female ovary and uterus cDNA, RIKEN full-length
enriched library, clone:5031410123 product:VON WILLEBRAND FACTOR A-
RELATED PROTEIN homolog).
         TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously; NIH MGC Project;
                                                                                                                                                                                                                                                                                           STRAIN=Czech II,
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBR2Z5 MOUSE
QBR2Z5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50853; FN3; 2. PROSITE; PS50234; VWFA; 1. SEQUENCE 445 AA; 46804
                                      NUCLEOTIDE
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SM00327; VWA;
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EMBL/GenBank/DDBJ databases
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Pred. No. 2.7e-72;
; Mismatches 0;
                                                           99:16899-16903 (2002)
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RAWAIJ, Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Alakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Akadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kasukawa T., Saito R., Kadota K., Matsuda H., Shibata Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T., Sakai K., Oxido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Oxido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Oxido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Hofmann M., Fujita M., Gariboldi M., Sakai K., Oxido T., Fletcher C., Fujita M., Gariboldi M., An Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., An Brownstein M., Fletcher C., Fujita M., Gariboldi M., An Brownstein M., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., An Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Waysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Landard M., Yoshida K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Landard M., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Landard M., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Landard M., Kohtsuki S., Landard M., Kohtsuki S., Landard M., Kohtsuki S., Landard M., Kohtsuki S., Kawaji H., Kohtsuki S., Landard M., Kohtsuki S., Landard M., Kohtsuki S., Landard M., Kohtsuki S., Kawaji H., Kohtsuki S., Landard M., Kohtsuki S., Kawaji H., Kohtsuki S., Landard M., Kohtsuki S., Landard M., Kamada Y., Kawaji H., Kohtsuki S., Landard
STRAIN-C57BL/6J; TISSUE-Ovary and uterus;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya
Kurihara C., Matsuyama T., Miyasaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Ovary and uterus; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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Meth. Enzymol. 303:19-44(1999)
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                    NUCLEOTIDE
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Best Local (
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Von Willebrand factor A-related protein.
Name=Vwal; Synonyms=4932416AllRik, Warp;
                                                                                                                                           FEBS Lett. 517:61-66(2002).
EMBL; AY030094; AAK38350.1; -; mRNA.
HSSP; P18614; 1MHP.
                                                                                                                                                                                                               MEDLINE=22057805; PubMed=12062410; DOI=10.1016/S0014-5793(02)02579-6; Fitzgerald J., Ting S.T., Bateman J.F.; Fitzgerald J., Ting S.T., Bateman J.F.; WARP a new member of the von Willebrand factor A-domain superfamily of extracellular matrix proteins.";
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SMART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50234; VWFA; 1.
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InterPro; IPR002035; VWF A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
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EMBL; AK077240; BAC36703.1;
EMBL; BC036166; AAH36166.1;
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STRAIN=FVB/N; TISSUE=
Director MGC Project;
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nsembl; ENSMUSG00000042116; Mu8 m
GI; MGI:2179729; 4932416A11Rik.
GI; MGI:2179729; Vwa1.
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GO:0005615; C:extracellular space; TAS
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Muridae; Murinae;
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Pred. No. 7.5e-60
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, Hayashizaki
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Pfam; PF00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; PN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; PN3; 2.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44737 MW;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length (
library, Clone:4932416A11 product:VON WILLEBRAND FACTOR PROTEIN homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=99279253; PubMed=10349636;
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                            "Functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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MGI; MGI:2179729; Vwal.
GO; GO:0005615; C:extracellular sg
InterPro; IPR003961; FN III.
InterPro; IPR003961; VWF A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
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Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
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MEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0453; VWFADOMAIN SMART; SM00060; FN3; 2. SMART; SM00327; VWA; 1.
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                                                                                                                                                                                                                                                       Similarity
                                                                                                                                   PS50853; FN3; 2.
PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENSMUSG00000042116; Mus musculus.
                                   SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSDPV
                                                                                                   QGDLLFLLDSSASVSHYEFSRVREFVGQLVATMSFGPGALRASLVHVGSQPHTEFTFDQY
415 AA;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                44681 MW;
                                                                                                                                                                                                                                                       84.1%;
83.3%;
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                                                                                                                                                                                                                                   Score 768; UD ...
No. 1.7e-59;
                                                                                                                                                                                                                                                                                                                                                    CE137963B76834FE CRC64;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              space;
                                                                                                                                                                                                                                                                                    Length 415;
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Q642A6
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DC Mammall
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OC Murida
OC Murida
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RA Altsch
RA Altsch
RA Hopkin
RA Richar
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Deters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA secuences."
                                                                                                                                                                                                                                                                    Matches 150;
                                                                                                                                                                                                                                                                                                                             Query Match
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MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Von Willebrand factor A do Name=RGD1311476_predicted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00453; VWFADOMAIN SMART; SM00060; FN3; 2. SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC081983; AAH81983.1; -; mRNA. InterPro; IPR003961; FN III. InterPro; IPR0030361; FN _II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Von Willebrand factor A domain-related protein.
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Q642A6;
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                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50853; FN3; 2.
PS50234; VWFA; 1
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                                 $$GEAAQDAVRA$AQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGS$DPV
                                                                                                                                                                     RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLFLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                   QGDLLFLLDSSASVSHYEFSRVREFVGQLVATMPFGPGALRASLVHVGSRPHTEFTFDQY
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                                                                                                                                                                                                                                                                                               Score 761; DB 2;
Pred. No. 7.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                    B3A0A0268DB06D4E CRC64;
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        RESULT 7
Q4SD22_TETNG .
ID Q4SD22_TETNG PRELIMINARY;
AC Q4SD22;
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,

RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roset Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"The early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14659, whole genome shotgun sequence.
ORFNames=GSTENG00020556001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodonti
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
-I- CAUTION: The sequence shown here is derived from an
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preliminary data.
preliminary data.
cAAE01014659; CAG01701.1;
cAAE01014659; S3316 MW;
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                                                                                                                                                                                                                                                                                                                                                       D 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQSSLQGSLRNIKPLRGDTNTVEALKVAQERVLRPGVPGGARAGLPRVLVWLTDGVNPGD
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Pred. No. 1.5e-26;
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C724FA399E0751FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT 8
Q4SXE3_TETNG
ID Q4SXE3_TETNG
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RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Nicaud S., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Dasilva C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Ralis M., Volff JN., Guigo R., Somy M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

RT The early vertebrate proto-karyotype.";
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Matches
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                      Collagen;
NON_TER
NON_TER
SEQUENCE
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Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, Chromosome 14 SCAF14645, who
                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00453; VWFADOM/
SMART; SM00060; FN3; 11.
SMART; SM00327; VWA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00041; fn3; 11. Pfam; PF00092; VWA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope; Whitehead Institute Centre Submitted (FEB-2004) to the EMBL/GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00014; FNTYPEIII. PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CAAE01014645; CAG01460.1; -;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=99883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
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                                                                                                                                                                                         1 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                              l Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  PS50853; FN3; 12.
PS50234; VWFA; 3.
HILEAVVTALRTFPYRGGSTNTGRAMTYVRETVFQASRGARAHVPRVTILITDGKSSDAF
                                                                                                             SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
                                                                                                                                                       QADVVLLVDGSYSIGLANFAKVRAFLEVLVNTFDIGPDKVQISLVQYSRDPHTEFYLDSH
                                     GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI
                                                                                                                                                                                                                                                                                                                                                                  Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003961; FN III.
IPR003962; Fn III_s
                                                                                                                                                                                                                                                                                                          1723
1723
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                                                                                                                                                                                                                                                                                                                              1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWF_A.
                                                                                                                                                                                                                              30.0%; Score 273.5;
37.4%; Pred. No. 5.26
tive 28; Mismatches
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                                                                                                                                                                                                                                                                                                          MW;
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Last annotation update)
ole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome
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                                                                                                                                                                                                                                                                                                                                                                  Structural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic_DNA.
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                                                                                                                                                                                                                                                  .2e-15
                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                  protein
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 614
                                                                             555
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PRELIMINARY;

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Query
Best L
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InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003129; Laminin G TSP_INTERPO; IPR001220; Lectin_TegB.
InterPro; IPR001220; Lectin_TegB.
InterPro; IPR002035; VWF A.
Pfam; PP01391; Collagen; 2.
Pfam; PP00041; fn3; 8.
Pfam; PP00041; fn3; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraod. Tetraodontoidea; Tetraodontidae; Tetraodontoidea; Tetraodontidae; Tetraodontoidea; Tetraodontidae; Tetraodontoidea; Tet
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13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
Chromosome undetermined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50853; FN3; 9.
PROSITE; PS00307; LECTIN
PROSITE; PS50234; VWFA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00453; VWFADOMAIN
SMART; SM00060; FN3; 9.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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COEA1_CHICK STANDARD P32018; Q6LBL0; 01-UUL-1993 (Rel. 26, C 01-OCT-1996 (Rel. 34, I 13-SEP-2005 (Rel. 48, I COllagen alpha 1(XIV) Name=COL1441;

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Best Local :
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodo

Tetraodontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot i Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segu
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13-SEP-2005 (TrEMBLrel. 31, Last sequel
13-SEP-2005 (TrEMBLrel. 31, Last annot
Chromosome 10 SCAF15009, whole genome
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Q4RP12;
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MEDLINE=99280705; PubMed=10350466; DOT=10.1021/bi9900222;
Montserret R., Aubert-Foucher E., McLeish M.J., Hill J.M., Ficheux I Jaquinod M., van der Rest M., Deleage G., Penin F.;
Jaquinod M., van der Rest M., Deleage G., Penin F.;
"Structural analysis of the heparin-binding site of the NC1 domain collagen XIV by CD and NMR.";
Biochemistry 38:6479-6488(1999).
-!- FUNCTION: An adhesive role by integrating collagen bundles. It i probably associated with the surface of interstitial collagen fibrils via COL1. The COL2 domain may then serve as a rigid arm which sticks out from the fibril and protrudes the large N-terminal globular domain into the extracellular space, where it might increase with the extracellular space, where it
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Submitted
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Trueb J., Trueb B.;
"Type XIV collagen is a variant of
"Type XIV sollagen." 207:549-557(1992)
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Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
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Matrix Biol. 17:145-149(1998).
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MEDLINE=98357967; PubMed=9694594;
GITY-Lozinguez C., Aubert-Foucher
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MEDLINE=92037585; PubMed=1935930;
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SIMILARITY: Belongs to the fibril-associated collagen interrupted helices (FACIT) family.
SIMILARITY: Contains 8 fibromectin type-III domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
SIMILARITY: Contains 2 VWFA domains.
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                                                                                       Swiss-Prot entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation and the Company of the Swiss Institute of Bioinformatics are no restrictions on the Swiss Institute of the Swiss are not restricted to the Swiss Institute of the S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELJULAR LOCATION: Extracellular matrix.

UE SPECIFICITY: Wide tissue distribution, high presence in UE SPECIFICITY: Wide tissue distribution, high presence in Connective tissue in skeletal muscle.

Lysines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in all cases and bind carbohydrates.

Prolines at the third position of the tripeptide repeating Prolines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in some or all of the chains.
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st M., Mayne R., Olsen B.R.;
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PDB; 189Q; NMR; A=1853-1885.
InterPro; IPRO08160; Collagen.
InterPro; IPRO03961; FN_III.
InterPro; IPRO0395; VWF_A.
Pfam; PF001391; Collagen; 4.
Pfam; PF00041; fin; 8.
Pfam; PF00092; VWA; 2.
Pfam; PF00092; VWA; 2.
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PROSITE; PS50834; VWFA; 2.
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on 2 (COL1).
(Potential).
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PIM:

Prolines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in some or all of the chains. O-glycosylated; glycosaminoglycan of chondroitin-sulfate t

glycosaminoglycan

type

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RA Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.; Truege and small splice variants of collagen XII: differential Texpression and ligand binding.";

IJ. Cell Biol. 130:1005-1014(1995).

C containing fibrils, the COL1 domain could be associated with the courant of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrilar matrix.

1-1- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences.

1-1- ALTERNATIVE PRODUCTS:

Event=Alternarium ---
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Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Calliformes; Phasianidae; Phasianinae;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifs, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-White leghorn;
STRAIN-White leghorn;
MEDLINE-92011862; PubMed-1918137; DOI=10.1083/jcb.115.1.209;
Vamanata M.. Yamada K.M., Yamada S.S., Shinomura T., Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamagata M., Yamada K.M., Yamada Nishida Y., Obara M., Kimata K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93042014; PubMed=1420368; DOI=10.1016/C
Trueb J., Trueb B.;
Trueb J., Trueb B.;
"The two splice variants of collagen XII share
Biochim. Biophys. Acta 1171:97-98(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon M.K., Gerecke D.R., I "Type XII collagen. A large to type IX collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type IX collagen, and short collagenous domains
site.";
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                                          IsoId=P13944-2; Sequence=VSP_001148; TISSUE SPECIFICITY: Type XII collagen is pre ligaments, perichondrium, and periosteum, al tissues containing type I collagen.
DOMAIN: This sequence defines five distinct helical domains (COL1 and COL2) and three no
                                                                                                                                                                                                                                                                  Event=Alternative splicing, Named isoforms=2;
Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or an
combination of isoform Long and isoform Short. Only isofor
is a proteoglycan. Isoform Long has more restricted expres
domains (NC1, NC2, and NC3). PTM: The triple-helical tail is
                                                                                                                                                                                                                          Name=Long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=3476925;
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ct extracellular matrix component
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Pfam; PF01391; Collagen; 4.
Pfam; PF00041; fn3; 17.
Pfam; PF00092; VWA; 4.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
PROSITE; PS50853; FN3; 18.
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EMBL; X61024; CAA43358.1;
EMBL; M7375; AAA489718.1;
EMBL; M05137; AAA48655.1;
EMBL; X67327; CAA47744.1;
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REGION
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Alternative splicing; Cell adhesion; Collagen;
Direct protein sequencing; Extracellular matrix; Glycoprotein;
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SIMILARITY: Contains in
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SIMILARITY: Contains 1 TSP N-terminal
SIMILARITY: Contains 4 VWFA domains.
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similarity).
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089029; 089030; Q90MS3;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation updat
FEBS DECL. ...
[2]
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM DANGE).
STRAIN=C57BL/6J; TISSUE=Mammary gland;
STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; Peingold E.A., Grouse L.H., Derge J.G.,
Chranaberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler
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                                                                                                                                                                NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT), AND VARIANTS. STRAIN-C57BL/6J, and CD-1; TISSUB-Fetal; MEDLINE=98442849; PubMed=9771906 DOI=10.1016/S0014-5793(98)01111-9; Wagener R., Kobbe B., Paulsson M.; "Matrilin-4, a new member of the matrilin family of extracellular
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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T -> S (in Ref. 4).
D -> E (in Ref. 4).
P -> A (in Ref. 2).
L -> F (in Ref. 2).
V -> F (in Ref. 2).
QP -> AG (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 265.5;
Pred. No. 5.2e
33; Mismatches
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O-linked (Xyl...
(Potential).
O-linked (Xyl...
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O-linked (Xyl. . .) (chondroitin su
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Arg/Lys-rich (basic).
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les 83;
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    .) (chondroitin sulfate)

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Droc Maria M. A.; Tona S. C. (1000)
                                                                                InterPro; IPR000152; ABX hydroxyl_S.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR011203; Matn_vMA.
InterPro; IPR011203; Matn_vMA.
InterPro; IPR001255; VWF_A.
Pfam; PF00008; EGF; 4.
Pfam; PF000092; VWA; 2.
Pfam; PF00092; VWA; 2.
PRINTS; PR00453; VWA; 1.
PRINTS; PR00453; VWA; 1.
PROSITE; PS0010; ASX_HYDROXYL; 2.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01026; EGF 3; FALSE NEG.
PROSITE; PS00234; VWFA; 2.
Alternative sp
Polymorphism;
SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ006140; CAA06889.1;
EMBL; AJ006140; CAA06890.1;
EMBL; BC036558; AAH36558.1;
EMBL; AJ010984; CAA09451.1;
HSSP; P00736; 1APO.
                                                                                                                                                                                                                                                                                                         MGI; MGI:1328314; Matn4.
GO; GO:0005615; C:extracellular space; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
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1 :
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FEBS Lett. 438:165-170(1998).
-!- FUNCTION: Major component of the extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 218-257.
MEDLINE=99043241; PubMed=9827539;
                                                                                                                                                                                                                                                                                                                                               Ensembl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic organisation, alternative splicing and primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOId=089029-2; Sequence=VSP_001401;
TISSUE SPECIFICITY: Lung, brain, sternum, kidney and heart.
DEVELOPMENTAL STAGE: The short isoform was detected in 7 we mice but not in developing mice (19.5 dpc embryos or in 2, 21 days old animals).
SIMILARITY: Contains 4 EGF-like domains.
SIMILARITY: Contains 2 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cartilage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swiss-Prot entry is copyright. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=089029-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Puol
                                                                                                                                                                                                                                                                                                                                             ENSMUSG00000016995; Mus musculus.
splicing; Coiled coil; EGF-like
m; Repeat; Signal.
Potential.
22 624 Matrilin-4.
36 215 VWFA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its
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; mRNA.
; mRNA.
; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      way modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is produced through
                                                                    domain; Glycoprotein;
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Matches 64
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13-SEP-2005
13-SEP-2005
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COILED
CARBOHYD
CARBOHYD
DISULFID
Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard C., Skalli Z., Cattolico L., Poulain J., De Berardinis V. Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
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63 TETNG
Q4SH63_
                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=GSTENG00018311001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metozoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Acatinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TYEMBLrel. 31, Created)
13-SEP-2005 (TYEMBLrel. 31, Last sequence update)
13-SEP-2005 (TYEMBLrel. 31, Last annotation update)
13-SEP-2005 (TYEMBLrel. 31, Last annotation update)
Chromosome 8 SCAF14587, whole genome shotgun sequence.
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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By similarity.
328
By similarity.
349
By similarity.
355
By similarity.
364
By similarity.
365
By similarity.
367
By similarity.
368
By similarity.
379
Missing (in isoform Short).
/FIId=VSP_001401.
A -> E (in strain C57BL/6J).
DFA28D2C94B1A14F CRC64;
360
370
380
381
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382
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384
385
By similarity.
385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc. N-linked (GlcNAc.
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                                                                Robinson-Rechavi
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Best Local S
Matches 61
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SMART; SM00060; FN3; 6.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 2.
PROSITE; PRS0853; FN3; 7.
PROSITE; PRS0234; VWFA; 2.
Collagen; Extracellular matrix; S
Corby N.;
Corby N.;
Submitted (MAY-2005) to the
Submitted (MAY-2005) to the
EMBL; AL354664; CAH71309.1;
EMBL; AL354664; CAH713897.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K2 HUMAN
Q5VYK2 HUMAN
Q5VYK2;
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NON TER
SEQUENCE
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submitted (FEB-2004) to th
-!- CAUTION: The sequence
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                     Collagen, type XII, alpha 1.
Name=COL12A1; ORFNAmes=RP1-238D15.1-003;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2005 (TrEMBLrel. 29,
01-FEB-2005 (TrEMBLrel. 29,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 6. Pfam; PF00092; VWA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
EMBL; CAAE01014587; CAG00019.1;
InterPro; IPR008160; COllagen.
InterPro; IPR003961; FN_III.
                                                                                                                 NUCLEOTIDE
                                                                                                                                                                  Submitted
                                                                                                                                                                                                              NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
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InterPro; IPR002035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE
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| :|:: | :| :| | | | | | :::|: | | :| ::|
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                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003129; Laminin_G_TSP_N.
IPR002035; VWF_A.
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ON: The sequence shown
                                                                                                                                                                                                                                                                  (MAY-2005)
                                                                                                                                                                  (MAY-2005)
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                                                                                                                 SEQUENCE
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          EMBL/GenBank/DDBJ
-; Genomic_DNA.
-; Genomic_DNA.
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Last
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                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 265; DB 2;
Pred. No. 2.6e-14;
8; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence up
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hotgun (WGS)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                  databases
                                                                                                                                                                                                                                                                  databases
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                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry which
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88888

Ensembl;

+

localized in the perifibrill SUBUNIT: Trimer of identical nontriple-helical sequences. ALTERNATIVE PRODUCTS:

of the

fibrils,

ibrils, and the COL2 and NC3 domains perifibrillar matrix (By similarity) of identical chains each containing 1

domains may be

190 kDa

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cel1

collaboration L outstation -

18

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InterPro; IPRO0356; COllagen.

R InterPro; IPRO03161; FN III.

R InterPro; IPRO03129; Laminin_G_TSP_N.

InterPro; IPRO03129; VWF_A.

R InterPro; IPRO02035; VWF_A.

R Pfam; PF00191; Collagen; 2.

R Pfam; PF00041; fn3; 18.

R Pfam; PF00092; VWA; 4.

R Pfam; PF00093; VWFADOMAIN.

SMART; SM00060; FN3; 18.

R SMART; SM00010; TSPN; 1.

RR SMART; SM00327; VWA; 4.

RR SMART; SM00327; VWA; 4.

RR SMART; PS50853; FN3; 18.

RROSITE; PS50234; VWFA; 4.

COllagen; Extracellular matrix; Repeat; Structural protein.

COllagen; Extracellular matrix; Repeat; Structural protein.

SEQUENCE 2884 AA; 315869 MW; 2D598F13656E454D CRC64;
chromosome 6q12-q13.";
Genomics 41:236-242(1997).

-i- FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COL1 domain could be associated with the
                                                                     SEQUENCE.

MEDLINE=97288521; PubMed=9143499; DOI=10.1006/geno.1997.4638;
Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.;
"Complete primary structure of two splice variants of collagen XII,
and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX)
collagen (COL19A1), and alpha 1(XIX) collagen (COL19A1) to human
                                                                                                                                                                                                                                                                                                             GOCAL HUMAN STANDARD; PRT; 3063 AA. Q99715; Q99716; 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Collagen alpha 1(XII) chain precursor.
Name=COL12A1;
                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0005737; C:cytoplasm; IEA.
GO:0005578; C:extracellular matrix (sensu Metazoa);
GO:0005198; F:structural molecule activity; IEA.
GO:0007155; P:cell adhesion; IEA.
GO:0006817; P:phosphate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL096771; CA119907.1; -; Genomic DNA.
AL080250; CAH71309.1; JOINED; Genomic DNA.
AL0802571; CAH71109.1; JOINED; Genomic DNA.
AL354664; CA119897.1; JOINED; Genomic DNA.
AL080250; CA119907.1; JOINED; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPÄETHVFTVEDFDAFQRISFELTQSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI
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                                                                                                                                                                                             SEQUENCE (ISOFORMS LONG AND SHORT), AND PARTIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.9%;
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Pred.
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No. 7.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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            InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
Pfam; PF01391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWA; 4.
          SIGNAL
CCHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U73778; AAC51244.1; -;
EMBL; U73779; AAD40483.1; -;
HSSP; P18614; IMHP.
                                                                                                                                                                                                                                                                              Alternative splicing; Cell adhesion; Collagen; Direct protein sequencing; Extracellular matrix;
                                                                                                                                                                                                                                                                                                             PRINTS; PR00453; VWFADOMAIN.
PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; VWFA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSG00000111799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005595; C:collagen type XII; TAS.
GO; GO:0001501; P:skeletal development; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC; HGNC:2188; COL12A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collagen interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
PTM: O-glycosylation of isoform Long; glycosaminoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        each end (By similarity).

PTM: Prolines at the third position of the tripeptide unit (G-X-Y) are hydroxylated in some or all of the cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q99715-2; Sequence=VSP_001149; IISSUE SPECIFICITY: Found in collagen I-containing tissues isoform Short and isoform Long appear in amnion, chorion, muscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the isoform is found in lung, placenta, kidney and a squamous carcinoma cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing, Named isoforms=2;
Comment=The final tissue form of collagen XII
homotrimers of either isoform Long or isoform
combination of isoform Long and isoform Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q99715-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                 /lation;
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                                                                                                                                                                                                                                                              Repeat;
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                                         Fibronectin VWFA 3.
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VWFA 2.
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Query Match Best Local (

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             2006,
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Nonhelical region (NC1).

Cell attachment site (Potential).

Hydroxyproline (By similarity).

N-linked (GlcNac. . .) (Potential).

O-linked (Xyl. . .) (chondroitin sulf
                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                        O-linked (Xyl...) (chondroi (Potential).
O-linked (Xyl...) (chondroi (Potential).
N-linked (GlcNAc...) (Poten Missing (in isoform Short).
/FTId=VSP 001149.
                                                                                                                                                                                                                                                                                          MW;
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VMFA 4
TSP N-terminal.
Nonhelical region (
Triple-helical region (
                                                                                                                                                                                                                                  Score 263.5; DB 1;
Pred. No. 7.7e-14;
0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               imperfection.
Nonhelical region (NC2).
Triple-helical region (COL1) with
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
O-linked (X
               07:47:45
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region (COL2)
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Result
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-Q=/abss/ABSSWEB spool/US10699035/runat 13022006 062440 25443/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006 062440 25443/app_query.fasta_1
-DB=A_Geneseq_-OFMT=fastan -SUFFIX=rag'-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US10699035 @CCN 1 1 476 @runat 13022006 062440 25403 -NCPU=5 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
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Maximum DB
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Perfect score:
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seq length: 2000000000
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Ygapop 10.0 , X
Ygapop 6.0 , F
Gapop 6.0 , F
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1: geneseqp19
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2380
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Abp69674 Human pol
Adh71106 Human pro
Aae32501 Mouse Wil
Aaw86326 Kidney in
Aab88340 Human mem
Ady63045 Human clo
Aab42581 Human ORF
Aab87344 Human gen
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ALIGNMENTS

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RESULT 1
AAE32502
                      Disulfide-bond
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                                                                                    Misc-difference
                                                                                                                               Protein
                                                                                                                                                               Key
                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                    Human Willebrand Factor A domain related-protein (WARP).
                                                                                                                                                                                                                                                                         24-MAR-2003 (first entry)
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                     Modified-site
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                                                                                                                                                   Peptide
                                                                                                                                                                                                          human.
                                          /note= "N-glycosylation site"
359
                                                                                    /note= "O-glycosylation site"
210. .211
                     /note= "N-glycosylation site"
361
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 369.
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                                                                                                                    /note=
                                                                                                                                       /label=_Signal_peptide
         note= "0-glycosylation site"
                                                                         note= "Encoded by CTCGCG"
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                                                                                                                   "Human mature WARP protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human WARP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated Willebrand Factor A-Related Protein polypeptide useful for manufacture of a medicament in the treatment of a disease condition the extracellular matrix, in particular arthritis.
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                                     AAGGAACAGCTGTTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTG
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                                                                                                                                                            Page 76-78; 103pp;
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ABP69674 protein; 445

ABP69674;

(first entry)

Human polypeptide SEQ ID NO 1721.

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; fungicide;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to an isolated polynucleotide (I) comprising a CC nucleotide sequence selected from any of 948 sequences (ABZ1119-CC ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for CC identifying expressed genes or for physical mapping of human genome. The CC encoded polypeptides (ABP68902-ABB69849) are useful as molecular weight CC markers, as a food supplement, for generating antibodies, in medical CC imaging, screening and diagnostic assays and for treating cell-CC proliferative disorders (cancer), neurodegenerative diseases (parkinson's CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis, CC diabetes, lugus) genetic disorders, myeloid or lymphoid disorders, liver CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic), CC arthritis, etc. Note: The sequence data for this pattent did not form part CC of the printed specification, but was obtained in electronic format CC directly from WIPO at.ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
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                              GTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGT
                                                                       AGCTCAGCCAGCGTCTCCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAGCTG
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2002US-0386376P
2002US-0386453P
2002US-0386664P
2002US-0386931P
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2002US-0386931P
2002US-0386971P
2002US-0387626P
2002US-0387610P
2002US-0387610P
2002US-0387610P
2002US-0387625P
2002US-0387635P
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2002US-0389742P
2002US-0389114P
2002US-0389144P
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2002US-0389144P
2002US-038914P
2002US-0389144P
2002US-0401489P
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113-AUG-2002

11
                                                                                                                         neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and antilipaemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
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N-PSDB;
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Rieger DK,
Smithson G,
Zhong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ; Catterton E, Chapoval A, Crabbree-Bokor JR, Edinger SR, Ellerman K; Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X; Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS; Paddigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L; Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA; Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NOVX polypeptides and nucleic acid molecules useful for preventing treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
                                             typing, preventive medicine, represents a NOVX polypeptid
                                                further used as hybridisation probes, in chromosome typing, preventive medicine, and pharmacogenomics. Trepresents a NOVX polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial,
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2002US-0403458P
2002US-0403459P
2002US-0403531P
2002US-0403531P
2002US-0403517P
2002US-0406182P
2002US-0406182P
2002US-0406182P
2002US-0406182P
2002US-0410840P
2002US-0412528P
2002US-0412528P
2002US-04112840P
2002US-0414830P
2002US-0414840P
2002US-0417186P
2002US-0417186P
2002US-0417186P
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2002US-0421369P
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Alignment & Pred. No.:

Scores:

7.85e-137 2114.00

Length: Matches:

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Query Match:
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Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP; gene therapy; mouse.
                                                    02-MAY-2001;
                                                                              02-MAY-2002;
                                                                                                                                                                         Disulfide-bond Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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Fitzgerald
                                                    2001AU-00004701
                                                                                2002WO-AU000542
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                                                                                                                                                                       /note= "O-glycosylation 369..393
                          CHILDRENS RES
                                                                                                                                                                                                                                                                      /note=
264
                                                                                                                                                                                                                                            /note= "N-glycosylation 359
                                                                                                                                                                                                                                                                                                                           /label= Signal_peptide
19. .415
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                            note= "0-glycosylation"
                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                             "N-glycosylation
                                                                                                                                                                                                                                                                                    "O-glycosylation site"
                                                                                                                                                                                                                                                                                                               "Mouse mature WARP protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain related-protein (WARP).
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y Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition in nolves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 415
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ATTGTCCAAGAGCTGAGGGGGCTCCATTCTC---
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                                                                                                                                                                                   CTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCTGTCAGCC
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                                                            Sanicola-Nadel M,
                                                                                                                                           23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kidney injury
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a kidney injury associated molecule (KIM) CC protein. KIM proteins can be administered therapeutically by expressing CC KIM encoding polynucleotides, to promote growth and/or survival of CC damaged tissue (e.g. renal tissue), since the KIM proteins are CC upregulated in injured or regenerating (especially renal) tissues. KIM CC dission proteins, conjugates, antibodies and vectors can also be used CC therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/CC prophylaxis of conditions associated with disfunction/disregulation of CC KIM genes or proteins, especially renal diseases or impairments of renal function in humans (e.g. acute renal failure, acute nephritis). The CC polynucleotides can be used to produce antisense sequences which, when internalled into cells, can disrupt expression of a cellular KIM gene, CC calso useful in therapy (e.g. to block the growth of tumours dependent on CC KIM for growth) or compositions. The proteins and polynucleotides are compositions. The proteins and polynucleotides are (indicative of increased risk, or presence of, renal injury or impaired CC (increased risk, or presence of, an autoimmune response or abnormal tissue growth arising from/affecting renal tissue). The proteins can also be CC used to locate KIM-producing cells (especially specific loci, e.g. tissue masses abnormally producing/expressing KIM such as tumours arising tissue in a dispression reader and imagina readers accountails with an imageable KIM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kidney injury-associated molecule, KIM, injured or regenerating tissues, useful regeneration, especially to treat renal
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binding reagent and imaging reagent
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Human; secretory protein; membrane protein; vaccine; rheumatoid arthritis; diabetes.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane protesins represented by AAB8317
CC - AAB8419. Included in the invention are primers AAF93917 - AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the cinvention. The invention also includes methods for the production of the cantibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polymucleotide sequences can be used in gene cused in the prevention, treatment and diagnosts of diseases associated cused in the prevention, treatment and diagnosis of diseases associated concleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The colypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and contribute and in antibodies may also be used as therapeutic agents to down regulate expression and contributed inmunosorbant assay (EJISA). Examples of diseases which may be contributed in antibodies and arthritis and diabetes
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel human secretory proteins or membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
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02-APR-1999;
05-APR-1999;
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                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                               N-PSDB;
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;

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Alignment
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                                                                                          TGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATCAT
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                        TGTCCAAGAGCTGAGGGGCTCCATTCTC---GCGATGCGGCCGCAGCAGCTCCATGCCAC
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eValGlnGluLeuArgGlySerIleLeuAspAlaMetArgProGlnGlnLeuHisAlaTh
                                                                                                                                                                                       uGlyValThrValPheIleValSerThrGlyArgGlyAsnPheLeuGluLeuSerAlaAl
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AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be disgnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ni J, Baker KP,
Soppet DR, Young
Moore PA, Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                              preventing, treating Parkinson's diseases
                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules encoding human secreted p
preventing, treating or ameliorating a disorder,
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03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                  11; Page 532-533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF91860
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99US-0152317P.
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and cancers.
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Olsen HS, Lafleur DW;
                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, used in r, e.g. Alzheimer's
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Alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), seppis, diabetes, atherosclerosis, CC cardiovascular disorders, seppis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, cognitive disorders, related disorders, endocrine disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used CC as a food additive or preservative to modify storage properties. CC Antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked indumnosorbent assay (ELISA). The present sequence represents a human CC carrieted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 215
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                                                                          GCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATC
                                                                                                                                       TrpValThrAspGlyGlySerSerAspProValGlyProProMetGlnGluLeuLysAsp
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US-10-699-035A-5 (1-1254) x ABG65347 (1-215)
                                                                                                                                                                                                                                                Alignment
                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired limmunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
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ABG63326-ABG65518
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(ROSE/) ROSEN C A. (HASE/) HASELTINE
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2004-090519/09

New albumin fusion proteins, useful for diagnosing, treating, or ameliorating diseases or disorders e.g. cancer, anemia, ariasthma, inflammatory bowel disease or Alzheimer's disease. , treating, preventing anemia, arthritis,

Disclosure; SEQ ID NO 2096; 279pp; English

CC cardiant, notropic, antilpaemic, nephrotropic, uropathic, convergence antilpaemic, nephrotropic, uropathic, convergence antilpaemic, nephrotropic, uropathic, enabolic, convergence and vulnerary. The albumin fusion protein nucleic acid may convergence and vulnerary. The albumin fusion protein nucleic acid may convergence and vulnerary. The albumin fusion protein is convergence and protein is convergence and protein in the store and protein is convergence and protein indication: Y. The diseases or disorders include: cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), convergence convergence (e.g. nanemia, multiple myeloma, arthritis, asthma, AIDS, convergence and the store and Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay Sachs disease), excretory diseases (e.g. urinary incontinence, urinary tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis, cerebellar ataxia, attention deficit disorder, autism or obsessive compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, scleroderma, wound healing or epidermolysis bullosa). This sequence represents a therapeutic protein X relating to the albumin fusion protein of the invention. The sequence listing data for this specification was dowloaded from the USPTO website. disorder in a patient comprising the step of administering the albumin fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of extending the shelf life of Therapeutic protein: X, or its fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein and its compositions have the following activities: cytostatic, antiantemic, antiarthitic, antiasthmatic, antiarthitic, antiarthythmic, osteopathic, dermatological, antignout, immunomodulator, antiarrhythmic, cardiant noctronic, antilneemic, nephrotronic, uropathic, cardiant noctronic, antilneemic, perhyptoronic, uropathic, cardiant noctronic, antilneemic, perhyptoronic. further relates to: a composition comprising the albumin fusion pand a pharmaceutical carrier; a kit comprising the composition of albumin fusion protein formula; a method of treating a disease or relates to a novel albumin fusion protein.

Sequence

Percent Similarity: Best Local Similarity: Score: Query Match: 5.95e-65 1067.50 99.1% 99.1% Length:
Matches:
Conservative: Gaps: Mismatches: Indels:

US-10-699-035A-5 (1-1254) x ADL78614 (1-215)

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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                             Human gene 3
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                 31-AUG-2000; 2000WO-US024008.
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Ś 밁 Ś Best Local S Query Match:

US-10-699-035A-5 (1-1254) x AAB87418

(1-242)

Gaps:

Percent Similarity: Best Local Similarity:

6.09e-65 1067.50 99.1% 99.1% 44.9%

Length:
Matches:
Conservative:
Mismatches:
Indels:

Score: Alignment

No::

242

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GGCGCGAGCGCGCCCCCCAGCATCAGCCCCCCCGAGGGGACCTGATGTTCCTGCTGGAC

MetLeuProTrpThrAla***GlyLeuAlaLeuSerLeuArgLeuAlaLeuAlaArgSer ATGCTCCCCTGGACGGCCTCGGCCCTGGCCCTTGAGCTTGCCGCTTGGCGCTGGCGCGCGGAGC

GlyAlaGluArgGlyProProAlaSerAlaProArgGlyAspLeuMetPheLeuLeuAsp

181

GTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGT

240 87 180 67 120 47 60

 ${\tt SerSerAlaSerValSerHisTyrGluPheSerArgValArgGluPheValGlyGlnLeuren}$ AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGGAGTTTGTGGGGGCAGCTG á

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CA AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB873413 represent the protein fragments. The genes can their corresponding secreted protein fragments. The genes can their corresponding secreted proteins are useful for preventing, creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating medical conditions, e.g., by protein or gene creating or ameliorating the presence of mutations in the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the cannount of the new genes. Specific uses are described for each of the immune system, cannount of the immune system, ca
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Soppet
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03-SEP-1999;
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Shi Y, Wei
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Ebner R, Duan DR,
Y, Florence KA;
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Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers.
                                                             WPI; 2001-203081/20.
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                                                                                       Baker KP, Birse CE, Fiscella M, DR, Young PE, Ebner R, Duan DR, PA, Shi Y, Wei Y, Florence KA;
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밁 S 멍 ર્જ 뭐 Ş 밁 δ

Disclosure; Page 18; 607pp; English.

cc and their corresponding secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or gene cherapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the canonic of the new genes. Specific uses are described for each of the canonic of the canonic of the conditions of the conditions of the conditions of the conditions in the new genes. Specific uses are described for each of the canonic of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the canonic of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the products for the diagnosis or treatment of conditions. Allows a conditions of the disorders, diseases of the immune system, conditions, neurological disorders (e.g., reunmatoid arthritis), inflammation, conditions, disorders, diseases, conditions, disorders, stancophrenia, asthma, skin conditions, disorders, stancophrenia, asthma, skin conditions, disorders, and infections. The proteins can also be used to aid wound the aling and epithelial cell proliferation, to prevent skin aging due to conduct of primary tissues, to regenerate tissues, to identify their conditions of primary tissues, to regenerate tissues, to identify their conditions of primary tissues, to regenerate tissues, to identify their conditions of primary tissues, to regenerate tissues, to identify their conditions of primary tissues, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Cc alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radiommunoassay or enzyme linked communoassays e.g., radiommunoassay or enzyme linked conditions in the discrete of the invention conditions in the discrete of the invention con AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes

Sequence

Best Local Percent Similarity: ö Similarity: 1.44e-64 1062.00 100.0% 100.0% 44.6% Length:
Matches:
Conservative: Gaps: Mismatches: Indels: 226 210 0 0

á 문 S 밁 Ś Б ş 밁 Ś 뮺 Ş US-10-699-035A-5 (1-1254) x AAB87424 361 301 241 114 181 121 74 54 34 61 14 94 ۲ GlyAlaGl AAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTG GTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGCCTGGTCTATGCC CGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCGGGTGAGGCTGCCCAGGATGCG ValAlaProLeuProLeuGlyThrGlyAlaLeuArgAlaSerLeuValHisValGlySer GGCGCGGAGCGCCGCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGAC MetLeuProTrpThrAlaLeuGlyLeuAlaLeuSerLeuArgLeuAlaLeuAlaArgSer GTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGT SerSerAlaSerValSerHisTyrGluPheSerArgValArgGluPheValGlyGlnLeu AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCCGGGTTCGGGGAGTTTGTGGGGGCAGCTG ATGCTCCCCTGGACGGCGCTCGGCCCTGGCCCTTGAGCTTGCCGCTGGCGCTGGCGCGCAGC (1-226)53 33 420 133 360 113 300 240 73 120 93

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                    AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the protein in a sample or by determining the for each of the second on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
                                                                                                                                                                                                                                                                                                                                     Disclosure;
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  proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP, Birse CE, Fiscella M, DR, Young PE, Ebner R, Duan DR, PA, Shi Y, Wei Y, Florence KA;
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                                                                                                                                                                                                                                                                                                                                  Page 18;
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  disorders,
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  cancer, tumours,
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Olsen HS,
foetal
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  and developmental
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Lafleur
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RESULT 15
AAE32500
ID AAE3
XX
AC AAE3
AC AAE3
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DT 24-M
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DE Huma:

AAE32500 standard;

protein;

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24-MAR-2003

(first

entry)

Human von Willebrand Factor A (VA) domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc abnormalities, haematopoietic disorders, diseases of the immune system, CR AIDS, autoimmune diseases (e.g., rheumatoid arrhritis), inflammation, cg allergies, neurological disorders (e.g., Alzheimer's disease, inflammation, cg altergies, neurological disorders (e.g., Alzheimer's disease), cognitive disorders, schizophrenia, asthma, skin cd disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc cardiovascular disorders, angiogenic disorders, kidney disorders, cc gastrointestinal disorders, pregnancy-related disorders, andocrine cd disorders, and infections. The proteins can also be used to aid wound company and epithelial cell proliferation, to prevent skin aging due to comburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in chemotaxis or immunoassave or arthress linked above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                              ProAlaProAlaAlaSerSerGlyProGlyArg***ProSerArgGlyAla
                   CCAGCGCCAGCCGCAAGCTCAGGGCCAGGCCGAGCGCCGTCCAGGGGAGCA
                                                                    GlyThrSerGlyProLeuGlyGlyLeuMetLeuValAspArgAlaProArgArgSerAla
                                                                                    ProGlnThrProGluProGlyArgThrArgSerGluArgArgTrpLeuSerCysProAla
                                                                                                                                                          ArgAlaProAsgTrpHisAlaGlyProArgCysProGlyAlaValGluProProAlaAla
                                                                                                                                                                                                                                                                             GlyGlnProHisProSerCysAlaGlyArgArgGlyThrArgCysMetAlaAspCysPro
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                                                                                                                                                                                                    US-10-699-035A-5 (1-1254) x AAE32500
                                                                                                                                                                                                                                                                                                                                                               The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                      present sequence is human VA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 72-73; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-111873/10.
N-PSDB; AAD50397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001; 2001AU-00004701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP; gene therapy; human.
                                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MURD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w isolated Willebrand Factor A-Related Protein polypeptide useful for e manufacture of a medicament in the treatment of a disease condition the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                       Scores:
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                                                                                                                                                  AGCTCGGGTGAGGCTGCCCAGGATGCGGTGCGTTCTGCCCAGCGCATGGGTGACACC
                                              CGTGCCAGTCTGGTGGACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCAC
SerSerGlyGluAlaAlaGlnAspAlaValArgAlaSerAlaGlnArgMetGlyAspThr
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PheValAspValAspAspLeuHisIleIleValGlnGluLeuArgGlySerIleLeu
                  TTTGTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCCATTCTC
                                                                                                                    GlyProProMetGlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGly
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-NO_MMAP_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG_-DEV_TIMEOUT=120
-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6_-FGAPEXT=7
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Fgapop 6.0 , E
Delop 6.0 , I
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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| Publication No. US20040214349A1 |
| GENERAL INFORMATION: APPLICANT: Bateman, John |
| APPLICANT: Bateman, John |
| APPLICANT: Fitzgerald, David |
| TITLE OF INVENTION: A Molecular Marker |
| FILE REFERENCE: A36056 PCT USA A 071838.0142 |
| CURRENT APPLICATION NUMBER: US/10/699,035A |
| CURRENT FILING DATE: 2003-10-31 |
| PRIOR APPLICATION NUMBER: PCT/AU02/00542 |
| PRIOR APPLICATION NUMBER: BOT/AU02/00542 |
| PRIOR APPLICATION NUMBER: AU PR4701/01 |
| PRIOR APPLICATION HOMBER: BURNER: AU PR4701/01 |
| PRIOR APPLICATION HOMBER: BURNER: BURNE
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APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 4
LENGTH: 415
TYPE: PRT
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US-10-699-035A-4
                                                                                                     Sequence 4, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REPERENCE: A35056 PCT USA A 071838 0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 415
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ORGANISM: Mus musculus
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; Patent No. US20020064818A1
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; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; PRIOR FILING DATE: 1999-09-03
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
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TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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FEATURE:
NAME/KEY: SITE
LOCATION: (7)
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TYPE: PRT
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AlaAlaSerAlaProAlaGluLysHisLeuHisPheValAspValAspAspLeuHisIle
                                                                                                       AAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGGTGCCCAAAGTGCTGGTG
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               GCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATC
                                                                                                                                                              LysGluGlnLeuPheAlaGluAlaSerGlyAlaArgProGlyValProLysValLeuVal
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: X
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US-09-833-245-2096
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Pred. No.:
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR PPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
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SOFTWARE: Pater.
SOFTWARE: Pater.
FOR ID NO 2096
TENGTH: 215
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
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TYPE: PRT
ORGANISM: Homo
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Percent Similarity:
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Query Match:
DB:
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APPLICANT: Ni et al.

TITE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: P2043P1

CURRENT APPLICATION NUMBER: US/10/883,936

CURRENT FILING DATE: 2004-07-06

PRIOR APPLICATION NUMBER: US/09/789,561

PRIOR FILING DATE: 2001-02-22

PRIOR PRIOR APPLICATION NUMBER: PCT/US00/24008

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/152,317

PRIOR APPLICATION NUMBER: 60/152,317

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 194

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NUMBER: PATE: 194
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; OTHER INFORMATION: Xaa equals
US-10-883-936-85
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SEQ ID NO 85
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TYPE: PRT
ORGANISM: Homo &
FEATURE:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-789-561-159
; Sequence 159, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
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; LOCATION: (34)
; OTHER INFORMATION:
US-09-789-561-159
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; SEQ ID NO 159

; LENGTH: 242

; TYPE: PRT

; ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
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RESULT 9
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CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR PILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 159
LENGTH: 242
TYPE: PRT
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Publication No. US20050019866A1
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                                                                                FEATURE:
NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: >
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TITLE OF INVENTION: 52 Human secreted proteins
                            LOCATION: (5)
OTHER INFORMATION:
                                                                                                                                     ORGANISM: Homo
                                          NAME/KEY: SITE LOCATION: (5)
                                                                      FEATURE:
  NAME/KEY: SITE
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                                                                                                                                  Sequence 165, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
TITLE OF INVENTION: 52 Human secreted proteins FILE REFERENCE: P2043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
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Percent Similarity:
Best Local Similarity:
Query Match:
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; OTHER INFORMATION: Xaa equals US-10-883-936-159
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; PRIOR FILING DATE: 19:
; NUMBER OF SEQ ID NOS:
; SOFTWARE: PATENTIN Ve:
; SEQ ID NO 165
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapien:
US-09-789-561-165
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Query Match:
DB:
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US-10-883-936-165
; Sequence 165, Application US/10883936
; Publication No. US20050019866A1
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GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted prot
FILE REFERENCE: PZ043P1
CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
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; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION UNMBER: PCT/US00/24008
; PRIOR APPLICATION UNMBER: 60/152,317
PRIOR APPLICATION UNMBER: 60/152,317
; PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 165
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-883-936-165
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Query Match:
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RESULT 12
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 160
LENGTH: 186
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
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LOCATION: (186)
OTHER INFORMATION:
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NAME/KEY: SITE
LOCATION: (184)
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ORGANISM: Homo sapiens
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RESULT 13
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CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR PILLING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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TITLE OF INVENTION: 52 Human secreted proteins
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OTHER INFORMATION:
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LOCATION: (184)
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
FURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-699-035A-2
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TYPE: PRT
ORGANISM: Homo
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                                   ArgProGlyValProLysValLeuValTrpValThrAspGlyGlySerSerAspProVal
                                                                 CGGCCAGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTG
                                                                                           HisThrGlyLeuAlaLeuValTyrAlaLysGluGlnLeuPheAlaGluAlaSerGlyAla
                                                                                                                       CACACTGGCCTGGCGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCC
                                                                                                                                               SerSerGlyGluAlaAlaGlnAspAlaValArgAlaSerAlaGlnArgMetGlyAspThr
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature; OTHER INFORMATION: Incyte US-10-149-819-18
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US-10-149-819-18
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APPLICANT: YUE, Henry
APPLICANT: AZMEZAI, Yalda
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Cha
APPLICANT: BAUGHN, Mariah
APPLICANT: LU, Dyung Aina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/10149819
Publication No. US20030044913A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo &
FEATURE:
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APPLICANT: SHAH, Purvi
APPLICANT: LAL, Preeti
APPLICANT: AU-YOUNG, Janice
APPLICANT: BURFORD, Neil
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND
FILE REFERENCE: PF-0760 PCT
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            GTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCGGGTGAG
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LU, Dyung Aina M.
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Search completed: February 13, 2006, 13:53:31 Job time : 212.799 secs

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Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 0.5
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913
1 RGDLMFLLDSSASVSHYEFS.....FVDVDDLHIIVQELRGSILD 180
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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SUMMARIES .

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ALIGNMENTS

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The invention relates to Willebrand Factor A domain related protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal	Claim 7; Page 72-73; 103pp; English.	New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.	; 2003-111873/10. SDB; AAD50397.	Bateman JF, Fitzgerald DJ;	(MURD-) MURDOCH CHILDRENS RES INST.	02-WAY-2001; 2001AU-00004701.	02-MAY-2002; 2002WO-AU000542.	07-NOV-2002.	WO200288184-A1.	/note= "Encoded by CTC"	/note= "Encoded by GGG"	ier:	o sapiens.		extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP; gene therapy: human	Willebrand Factor A domain related-protein; von Willebrand Factor A; VA;	Human von Willebrand Factor A (VA) domain.	24-MAR-2003 (first entry)	AAE32500;	AAE32500 standard; protein; 180 AA.	

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Matches 180; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                      inmunne system disorder; AIDS; autoimmune disease; rheumatojoietic disorder; inflammation; allergy; neurological disorder; AIDS; attoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDAeimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 180
                             Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer, Parkinson's diseases and cancers.
                                                                                         WPI; 2001-203081/20.
N-PSDB; AAF91860.
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03-SEP-1999;
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Ebner R, Duan DR,
Y, Florence KA;
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GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD

SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120

SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV

151

211

RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 60

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CC AARS/1858-AARS/1829 represent courses contained the proteins they encode.
CC AABS7414-AABS7454 represent human secreted proteins fragments. The genes
CC AABS7414-AABS7454 represent human secreted proteins fragments. The genes
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC amount of the new protein in a sample or by determining the
CC and include developing products for the diagnosed by determining the
CC and include developing products for the diagnosis or treatment of
CC and include developing products for the diagnosis or treatment of
CC anterior and the seases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzhamer's diseases of
CC allergies, neurological disorders (e.g., Alzhamer's diseases,
CC ardiovascular disorders, cangiogenic disorders, sthrapphrenia, asthma, skin
CC disorders, and infections. The proteins can also be used to aid wound
CC disorders, and offictions. The proteins can also be used to aid wound
CC disorders, and pithelial cell proliferation, to prevent skin aging due to
CC gunburn, to maintain organs before transplantation, for supporting cell
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC alleviating symptoms associated with the disorders mentioned above, and
CC immunosorbent assay (ELISA). The present sequence represents a human
CC immunosorbent assay (ELISA). The present sequence represents a human
Query Match
Best Local S
Matches 180
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                                                                                        Sequence
  180;
                        Similarity
                                                                                                                                       protein of the invention
                                                                                           215
  Conservative
                                                                                           ΑΑ,
                      100.0%;
  0
                        Pred. No.
                                            Score 913;
  Mismatches
                           2e-94;
                                            DB 4;
    0
                                              Length 215;
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  0;
    Gaps
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Albumin fusion protein, therapeutic protein X; human albumin; I human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder;
                                                                                 cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                   27-AUG-2002
                                                                                                                                                                                                                                                                                              ABG65347 standard; protein; 215
                          Synthetic
                                                                     osteopathic;
                                         Homo sapiens
                                                                                                                                                                                                        albumin
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                        fusion
                                                                                                                                                                                                      protein #2022.
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Claim 11; Page 532-533; 607pp; English

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ADL78614
ID ADL7
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                                                             albumin fusion protein; cytostatic; antianaemic; antiarthritic; antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory; antipsoriatic; antibacterial; osteopathic; dermatological; antigout; immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic; nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquiliz; antidabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, dispetive disorders (e.g. Crohn's
                                                                                                                                                                                    Albumin fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endoorine disorders (e.g. diabetes), hammonodeficiency syndrome, AIDS), endoorine disorders (e.g. Alzheimer's, Parklinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis ABG63326-ABG65518 represent albumin fusion proteins of the invention
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 1935; 2102pp; English
                                                                                                                                                                                                                                                                                                                                                                      GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSDPV
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Pred. No. 2e-94;
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CC cardiant, noetropic, antilipaemic, nephrotropic, uropathic, cardiant, noetropic, antilipaemic, nephrotropic, uropathic, correlant, noetropic, antilipaemic, nephrotropic, uropathic, conversely, and vulnerary. The albumin fusion protein nucleic acid may CC hypertensive, and vulnerary. The albumin fusion protein is conversely to treat disorders. The albumin fusion protein is conversely to treat disorders. The albumin fusion protein is conversely to treat disorders. The albumin fusion protein is conversely to treat disorders. The albumin fusion protein is conversely to treat disorders. The albumin fusion protein is conversely to the albumin fusion protein in the converse or conversely to the albumin fusion protein is conversely to the albumin fusion protein in the converse or conversely to the albumin fusion protein adenocarcinoma or sertolicular disease, systemate lupus erythematosus, gout, muscular dystrophy conversely to the albumin fusion protein adenocarcinoma or sertolicular disease, particular disease, for the albumin fusion protein fusio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               albumin fusion protein formula; a method of treating a disease or disorder in a patient comprising the step of administering the albumin fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of extending the shelf life of Therapeutic protein: X, or its fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein and its compositions have the following activities: cytostatic, antianaemic, antiarthritic, antiasthmatic, antiarthritic, dermatological, antignut, immunomodulator, antiarrhythmic, osteopathic, dermatological, antianaemic, incontronic antiarrhythmic, antiarrhythmic antiarrh
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25-APR-2000;
21-DEC-2000;
                                                                                                                                 compulsive disorder), respiratory disease (e.g. emphysema, lung cancer occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, scleroderma, wound healing or epidermolysis bullosa). This sequence represents a therapeutic protein x relating to the albumin fusion protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New albumin fusion proteins, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 2096; 279pp; English.
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                                                                                                              represents a therapeutic protein X rela
of the invention. The sequence listing
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HASELTINE W A.
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(e.g. diabetes, Addison's
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AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the protein in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                 Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers.
                                                                                                                                                                                 Disclosure; Page 18; 607pp; English.
                                                                                                                                                                                                                                                                                                                  Moore PA,
                                                                                                                                                                                                                                                                                                                               Soppet
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03-SEP-1999;
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PA, Shi Y, Wei Y, Florence
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                er R, Duan DR, Florence KA;
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Pred. No. 2e-94;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                 Olsen HS,
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                                                                                                                                                                                                                                                                                                                                   Lafleur DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                    CA;
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AAB87418
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RESULT 6
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioinmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention
                                                                                                                                                                                                                                                                     foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abnormalities, haematopoietic disorders, diseases of the immune s AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammat allergies, neurological disorders (e.g., Alzheimer's disease, Parkinsons's disease), cognitive disorders, schizophrenia, asthma disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                       03-SEP-1999;
03-SEP-1999;
                                                                                                                31-AUG-2000;
                                                                                                                                                                                            WO200118022-A1
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disorders, cancer, tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; proliferative disorder; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded secreted
                                                                                                                2000WO-US024008
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                                                     99US-0152315P.
99US-0152317P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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Pred. No. 2.2e-94;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein fragment, SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation,
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(HUMA-) HUMAN

GENOME SCI INC

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RESULT 7
AAB88340
ID AAB8
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AC AAB8
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DT 23-M
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KW Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allargies, neurological disorders (e.g., Alzheimer's disease, CC allargies, neurological disorders (e.g., Alzheimer's disease, CC allargies, neurological disorders, schizophrenia, asthma, skin CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC disorders, and epithelial cell proliferation, to prevent skin aging due to constitute of primary tissues, to regenerate tissues, to identify their CC constelligands or binding partners, and in chemotaxis, and can be used CC as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked CC immunosorbent assay (ELISA). The present sequence represents a human CC secreted protein fragment referred to in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF91858-AAF91929 represent cDNAs corresponding to 52 human secret protein genes, and AAB87342-AAB87413 represent the proteins they (AAB87414-AAB87454 represent human secreted protein fragments. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 18; 607pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ni J, Baker KP,
Soppet DR, Young
Moore PA, Shi Y,
                                                          Human membrane or secretory protein clone PSEC0053.
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                                                                                                          23-MAY-2001
                                                                                                                                                                                           AAB88340 standard; protein; 285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Young PE, Ebner R, Duan DR,
Shi Y, Wei Y, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 913; DB 4; 100.0%; Pred. No. 2.4e-94; tive 0; Mismatches 0;
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Olsen HS, Lafleur DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 242;
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Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.

RESULT 8
ADY63045
ID ADY6
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AC ADY6

ADY63045 standard; protein; 285 AA

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ADY63045;

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                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development.
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02-MAY-2000; 2000JP-00183766.
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11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to nucleic acid sequences AAF93744 - AAF93916
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                                                                                                                                                                                                                                                                                                                                                                             treated include rheumatoid arthritis and
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                       GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEXHLHFVDVDDLHIIVQELRGSILD 180
                                                                                                                                                                                        RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                       SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
                                                                                                                                                                     RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                    285 AA;
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                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0
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609pp +
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                                                                                                                                                                                                                                                Score 913; DB 4
Pred. No. 3e-94;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                             diabetes
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02-JUN-2005

(first

entry)

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RESULT 9
AAE32502
ID AAE3
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AC AAE3
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DT 24-M
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DE Huma
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Best Local :
                                                                                                                                                                                                                                                                                     Matches 180;
                                                                                                                                                                                                                                                                                                                                                         membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
  Human Willebrand
                         24-MAR-2003
                                                 AAE32502
                                                                         AAE32502 standard;
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 48; 1240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polynucleotide encoding human membrane proteins, useful for examination and human secretary proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human clone PSEC0053 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REAS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to novel human secretory proteins
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                                                                                                                                                                                                                                                                                                                                      285
                                                                                                                                     GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                   GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                                                     SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                     SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                      RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                   RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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ilarity 100.0%;
Conservative (
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2000JP-00183766.
2000EP-00114090.
                         (first entry)
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  Factor
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                                                                         protein;
 A domain related-protein
                                                                          418
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Pred. No. 3e-94;
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diagnosis
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   (WARP)
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s of abnormality
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GPPMQELKDLGVTVFIVSTGRGNELELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD

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                                                                                                                                                                                The invention relates to Willebrand Factor A domain related-protein (MARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human WARP protein
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MURD-) MURDOCH CHILDRENS RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                     w isolated Willebrand Factor A-Related Protein polypeptide useful for se manufacture of a medicament in the treatment of a disease condition the extracellular matrix, in particular arthritis.
                                                                                                     180;
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 92
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                                                                                                                   Similarity
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                                                  RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                            418
                   SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
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                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
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                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                            103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "O-glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human mature WARP
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                                                                                                        0;
                                                                                                     Score 913; DB 6;
Pred. No. 5.2e-94;
; Mismatches 0;
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                                                                                                                               Length 418;
                                                                                                        Indels
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                                                                                                        Gaps
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152

GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD 211

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RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH

120 91

151

211 180 > 10.

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-CC ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences: The polynucleotides are useful for central protein or complementary sequences: The polynucleotides are useful for cencoded polypeptides (ABP68902-ABF69849) are useful as molecular weight cencoded polypeptides (ABP68902-ABF69849) are useful as molecular weight cencoded polypeptides (ABP68902-ABF69849) are useful as molecular weight considers, as food supplement, for generating antibodies; in medical consignation of the printed seases (Parkinson's cor alzheimer's disease), autoimmune diseases (multiple sclerosis, cor alzheimer's diseases), autoimmune diseases (multiple sclerosis, cor alzheimer's diseases, autoimmune, autoimmun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
  Matches 180;
                          Query Match
Best Local 9
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Xue AJ,
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multiple sclerosis; diabetes; genetic disorder; wound; burn; infect; arthritis; cytostatic; immunomodulator; notropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; aucoimmune disease; multiple disease; disease; aucoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 1721; 1012pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or coagulation disorders.
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                          Similarity
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T, Wang J,
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    Conservative
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Wa Y, Yamazaki V, Chen R,
, Wang D, Drmanac RT;
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Wang D,
                        100.0%;
  0;
                     Score 913; DB 5;
Pred. No. 5.7e-94;
    Mismatches
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l, Wang Z,
                                             Length 445;
    Indels
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Z, Ghosh
  0,
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RESULT 11
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11-JUN-
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vaccine; cancer; cachexia; Alzheimer's
obesity; diabetes; infectious disease;
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05-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; cytostatic;
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2002US-0389118P.
2002US-0389144P.
2002US-0389144P.
2002US-0389146P.
2002US-0389742P.
2002US-0389742P.
2002US-0389742P.
2002US-0389742P.
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2002US-0387859P.
2002US-0387933P.
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2002US-0388022P
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2002US-0387696P.
2002US-0387702P.
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2002US-0389123P.
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2002US-0387400P.
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2002US-0386931P.
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2002US-0386796P.
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2002US-0386047P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention NOV1a SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infectious disease; metabolic syndrome X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; nootropic;
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Alsobrook JP, Catterton E, Ettenberg S, Gusev VY, Herrmann JL, Ji v Maclachlan T, Malyankar UM, Padigaru M, Patturajan M, F <u>ن</u> Rothenberg ME, Sci Spytek KA, Stone Chapoval Gangolli Alvarez Per E, Anderson ...,

val A, Crabtree-Bokor JR, Edinger ...,

lli EA, Gerlach VL, Gorman L, Gunther

IJL, Ji W, Kekuda R, Li L, Liu X, N

/ Ankar UM, Meziok AJ, Millet I, Mishr

rajan M, Pena CEA, Peyman JA, Raha D,

berg ME, Sciore P, Shenoy SG, Shimket

k KA, Stone DJ, Vernet CAM, Voss EZ, Boldog FL, Casman SJ; xr JR, Edinger SR, Ellerman Gorman L, Gunther E, Guo X R, Li L, Liu X, Macdougall kana D, Rastelli L; Shimkets RA; Mishra VS; JR; 7

2004-081935/08

New treating NOVX polypeptides and nucleic acid molecules useful for preventing NOVX-associated disorders, e.g. cancer, diabetes, infection or and in chromosome mapping, tissue typing or pharmacogenomics. õ

SEQ ID NO 2; 1880pp; English.

neuroprotective, nootropic, anorectic, antidabetic, antimicrobial, and antilipaemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynuclectides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrob probes, chromosome mapping, tissue

Yue H, Baughn

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Burford N, P, Au-You

Azimzai Y, J,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; extracellular matrix and cell adhesion molecule; XMAD; gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; bown's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE03654 standard; protein; 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 typing, preventive medicine, and pharmacogenomics. represents a NOVX polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; nootropic; anticonvulsant; antithyroid; nephrotropic; dermatological.
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Pred. No. 5.7e-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC hybridisation probe useful in mapping the naturally occurring genomic CC sequences and to create knock in humanised animals (pigs) or transgenic CC animals (mice or rats) to model human diseases. Oligonucleotide or longer CC fragments derived from the polynucleotide sequences may be used as CC used for the diagnosis of disorders which specifically bind XMAD may be used for the diagnosis of disorders which specifically bind XMAD may be CC used for the diagnosis of disorder which specifically bind XMAD may be CC disease, prevented or treated include genetic disorders such as CC disease, mystonic dystrophy, Down's syndrome, cystic fibrosis, Gaucher's CC autoimmune/inflammatory disorders such as acquired immune deficiency CC syndrome (AIDS), Addison's disease, allargies, anaemia, athalassaenia, cCC atherosclarosis, Crohn's disease, diabetes mellitus, atopic dermatitis, CC glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis, CC osteoporosis, peoriasis, rheumatoid arthritis, ulcerative colitis, protozoal and helminthic infections and CC cander including breast, bladder, bone marrow, brain and uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagonist are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The polynucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally lethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders associated with expression of XMAD. They are also used for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative disorders.
                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nostropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                             AAB42581 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 111; 135pp; English.
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                                                                                                                                                                       (first
                                                                                                                            polypeptide
                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenocarcinoma, lymphoma, melanoma and myeloma
                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 892; DB 4;
Pred. No. 3.9e-92;
                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                 SEQ ID
                                                                                                                                 NO:4690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; noctropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; antivixal; antifungal; antitheumatic; antihyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs bott disease, cardiovascular disease, calabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
                                                                                                                                                      Matches 175;
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; ast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antianaemic; gene therapy; cancer; proliferative disorder; hyperte neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                                                                                               Sequence 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 3880-3881; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC76790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiviral; antibacterial; antifungal; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-)
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                                  63
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                                                                                                 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
                        GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP 122
                                                                           DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLAPXALRASLVHVGSRPYTEFPFGQHSS
GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP
                                                                                                                                                      Conservative
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99US-0127728P.
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                                                                                                                                                                    96.7%;
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                                                                                                                                                                      Score 883; DB 3
Pred. No. 8e-91;
                                                                                                                                                      Mismatches
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••
                                                                                                                                                                                        Length 299;
                                                                                                                                                      Indels
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PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD

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Best Local
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                                                                                                                                                                                                                                                                                   animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                          The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an
                                                                                                                                                                                                                                            Sequence 180 AA;
                                                                                                                                                                                                                                                                      present sequence is mouse VA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 78-79; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bateman JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2001; 2001AU-00004701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse von Willebrand Factor A (VA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MURD-)
                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolated Willebrand Factor A-Related Protein polypeptide useful for manufacture of a medicament in the treatment of a disease condition {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-111873/10.
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                                                                                                                                                                                 150;
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                                                                                                                                       RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
 GPPMQELKDLGVTIFIVSTGRGNLLELLAAASAPAEKHLHFVDVDDLPIIARELRGSITD
                  GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                             SSGQAIRDAIRVAPQRMGDTNTGLALAYAKEQLFAEEAGARPGVPKVLVWVTDGGSSDPV
                                                                           SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                      QGDLLFLLDSSASVSHYEFSRVREFVGQLVATMSFGPGALRASLVHVGSQPHTEFTFDQY
                                                                                                                                                                                 Conservative
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1. .2
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                                                                                                                                                                                                84.1%;
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                                                                                                                                                                                              Score 768; DB 6
Pred. No. 4e-78;
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                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                            6; Length 180;
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                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                    invention is
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                                    useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is mouse WARP protein
                                                                                                                                                                    The invention relates to Willebrand Factor A domain related-protein (WARR) which is a member of von Willebrand Factor A (VA) domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Willebrand Factor A-Related Protein polypeptide useful for
the manufacture of a medicament in the treatment of a disease condition
of the extracellular matrix, in particular arthritis.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-111873/10.
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 74-75; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MURD-) MURDOCH CHILDRENS RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200288184-A1
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359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "0-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "0-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "0-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Mouse mature WARP protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label=_Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "N-glycosylation site"
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Query Match
Best Local Similarity
Matches 150; Conserv

Conservative

84.1%; Score 768; DB 6; 83.3%; Pred. No. 1.3e-77; tive 14; Mismatches 16

16;

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Gaps

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Length 415;

Sear Job	뭣	8	B	Ş	D _D	Ş
rch co time						
mplet : 112	152	121	92	61	32	-
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US-10-699-035A-20
US-10-699-035A-31
US-10-699-035A-31
US-10-699-035A-21
US-10-699-035A-25
US-10-177-293-63
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US-10-301-822-26
US-10-474-794-257
US-10-639-035A-25
US-10-639-035A-27
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR TILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 2096
LENGTH: 215
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Best Local Similarity 100.
Matches 180; Conservative
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PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/.
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
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SEQ ID NO 85
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                TYPE: PRT
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FILING DATE: 2000-08-31
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                                    CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
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                                                                                                                                                                                                                                                                                                                    Sequence 165, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
SOFTWARE: P
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                                                                                                                                                                                                                                                   APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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TYPE: PRT
ORGANISM: Homo
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PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
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PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
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CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
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NAME/KEY: SITE
LOCATION: (7)
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                     PatentIn Ver.
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Pred. No. 1.9e-89;
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RESULT 7
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US-10-883-936-165
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PRIOR FILING DATE: 2001-02-22
PRIOR PPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR PPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 165
LENGTH: 226
                                                              GENERAL INFORMATION
                                                                                Sequence 159, Application US/09789561 Patent No. US20020064818A1
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Best Local Similarity
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GENERAL INFORMATION:
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APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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ORGANISM: Homo sapiens
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Pred. No. 2e-89;
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US-10-883-936-159
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CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR PILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
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CURRENT FILING DATE: 2001-02-22
FRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
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; SEQ ID NO 159
; LENGTH: 242
                                                                                                                                                                         SOFTWARE: PatentIn
SEQ ID NO 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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NAME/KEY: SITE
LOCATION: (2)
                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-09-03
                                                                                                                                    TYPE:
                                 NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                 ORGANISM: Homo sapiens
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ORGANISM: Homo
NAME/KEY: SITE
                                                                                               FEATURE:
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                                                                                                                                                      LENGTH: 242
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p. US20050019866A1
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                                     Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 2.2e-89;
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                                                                                                       RESULT 10
US-10-699-035A-20
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US-10-699-035A-6
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Sequence 20, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
APPLICANT: Bateman, John APPLICANT: Fitzgerald, David TITLE OF INVENTION: A Molecular Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10699035A Publication No. US20040214349A1
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Best Local Similarity 100.0%;
Matches 180; Conservative 0
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Best Local Similarity
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APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A MOLECular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: SITE
LOCATION: (34)
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2.2e-89;
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Pred. No. 4.7e-89;
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APPLICANT: INCYTE GENOMICS, I
APPLICANT: YUE, Henry
APPLICANT: AZIMZAI, Yalda
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandr
APPLICANT: BAUGHN, Mariah R.
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US-10-149-819-18
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Best Local Similarity
Matches 180; Conserv
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SEQ ID NO 18
LENGTH: 185
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                    Matches
                                                                                                     Query Match
Best Local Similarity
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Publication No. US20030044913A1
                                                                                                                                                                                   TYPE: PRT
ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incy
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                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BURFORD, Neil TITLE OF INVENTION: EXTRACELLULAR MATRIX AND FILE REFERENCE: PF-0760 PCT
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                    176;
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MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
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LU, Dyung Aina M.
SHAH, Purvi
LAL, Preeti
AU-YOUNG, Janice
BURFORD, Neil
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                                                                               97.7%; So ilarity 100.0%; I Conservative 0;
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                                                                                  Score 892; DB 4; ]; Pred. No. 2.7e-87; 0; Mismatches 0;
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; FEATURE:
; OTHER INFORMATION: VA domain from WARP US-10-699-035A-31
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US-10-699-035A-31
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                                                                                     NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 181
TYPE: PRT
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LENGTH: 180
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Best Local :
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TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 FCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/699,035A CURRENT FILING DATE: 2003-10-31 PRIOR APPLICATION NUMBER: PCT/AU02/00542 PRIOR FILING DATE: 2002-05-02 PRIOR APPLICATION NUMBER: AU PR4701/01 PRIOR FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
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PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
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                                                                   ORGANISM: Artificial Sequence
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Sequence 21, Application US/10699035A

Publication No. US20040214349A1

Publication No. US20040214349A1

Publication No. US20040214349A1

PERIOR APPLICANT: Bateman, John

APPLICANT: Bateman, John

APPLICANT: Fitzgerald, David

TITLE OF INVENTION: A Molecular Marker

FILE REFERENCE: A36056 PCT USA A 071838.0142

CURRENT APPLICATION NUMBER: US/10/699,035A

CURRENT FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: PCT/AU02/00542

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR FILING DATE: 2001-05-02
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TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR TILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
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US-10-699-035A-4
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US-10-699-035A-21
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
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Best Local Similarity
Matches, 150; Conserv
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TYPE: PRT
ORGANISM: Mus musculus
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83.3%; Pred. No. 1.7e-73;
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; Pred. No. 5.6e-74;
14; Mismatches 16
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Post-processing: Minimum Match 0%
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Maximum DB
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Issued Patents AA:*

1: /cgn2_6/ptcdata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptcdata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptcdata/1/iaa/RE_COMB.pep:*
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913
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Resul No	NO.	Score	Query Match	Length	B.	ID	Description
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	4	56.		755	Ŋ	-09-	equence 57,
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	ڼ	51.		915	N	-09-907-794	e 34,
	7	51.		915	N	-09-905-125A-3	equence 34,
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	9	51.		915	N	-09-	equence 34,
	10	51.		915	N	US-09-903-603A-34	equence 34,
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	21	51.		963	N	6-1152	11!
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	23	33.		496	ب	62-12	Sequence 37, Appl
	24	33.		496	ب	63-180-	37
	25	33.		496	ب	-08-001-078A	1
	26	33.	٠	496	ш	8-89	4,
	27	33.	25.6	496	щ	US-08-463-218-1	Sequence 1, Appli

233.5 25.6 496 4 PCT-US94-00253-1 231.5 25.6 496 2 US-09-914-259-34 227 24.9 405 2 US-09-914-259-34 224.5 24.6 481 2 US-09-914-259-36 214.5 23.5 486 2 US-09-914-259-35 214.5 23.5 486 2 US-09-949-016-6216 214.5 23.5 486 2 US-09-949-016-6216 214.5 23.5 1486 2 US-09-949-016-6216 214.5 23.5 20.7 2 US-09-949-016-6216 214.5 23.5 20.7 2 US-09-996-611D-2 198.5 21.7 171 2 US-09-996-611D-1 194 21.2 214 2 US-10-061-658-9 194 21.2 214 2 US-10-061-658-9 194 21.2 550 2 US-09-905-125A-227 194 21.2 550 2 US-09-905-775A-227 194 21.2 550 2 US-09-906-770-227 194 21.2 550 2 US-09-906-775A-227 194 21.2 550 2 US-09-906-775A-227 194 21.2 550 2 US-09-906-775A-227 194 21.2 550 2 US-09-906-700-227	45	44	43	42	41	40	39	38	37	36	ω G	ω 4	ω ω	32	31	30	29	0
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	2, Appli	227, App	227, App	227, App	227, App	9, Appli	6, Appli	1, Appli	2, Appli	9878, Ap	6216, Ap	278, App	•	36, Appl	374, App	34, App1	1, Appli	

ALIGNMENTS

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RESULT 2
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, NAME/KEY: UNSURE
; LOCATION: 66
; OTHER INFORMATION: Xaa=Cys or Gly
US-09-513-999C-6277
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6277, Application US/09513999C
                                                                                                               Sequence 10340, Application US/09949016
Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 76; Conserv
                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                77 MGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSDPVGPPMQELKDLGVTVFI
                                                                                                                                                                                                                                                                                                                   1 MGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFI 60
                                                                                                                                                                                                                                     VSTGRGNFLELSAAASA 153
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ilarity 98.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                               Score 384; DB 2;
Pred. No. 4.8e-36;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 77;
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LENGTH: 584
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10341
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-09-08
PRIOR FILING 
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US-09-949-016-10341
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: BOLYMORPHISMS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TYPE: PRT
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les 67; Conserv
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                                                                                                                                                                                                                                   GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP----GVPKVLVWVTDGGSSDP
                                                                                                                                                                                                                                                                                                                   DLVLLVDGSKSVRPQNFELVKRFVNQIVDFLDVSPEGTRVGLVQFSSRVRTEFPLGRYGT
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    ISVWAARAKEEGIVMYAVGVGKAVEAELREIASEPÄELHVSYAPDFGTMTHLLENLRGSI
                                                                       VGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.4%; Score 259; DB 2; Length 584; 37.2%; Pred. No. 1.5e-20; tive 25; Mismatches 84; Indels
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US-09-919-497-57
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US-08-897-443-1
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APPLICANT: MULTER, GEORGE L.
APPLICANT: MULTER, GEORGE L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION
PILE REFERENCE: B0801/7225
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 57
LENGTH: 755
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Patent No. 6773883
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Matches !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                      COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
ENTING APPLICATION NUMBER:
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APPLICANT: Hillman,
APPLICANT: Lal, Pre-
APPLICANT: Corley, 1
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TYPE: PRT
                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Ph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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REFERENCE/DOCKET NUMBER: PF
                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
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No. 5981263
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Shah, Purvi
Kaser, Mathew
                                                                                                                                                                                                                                                                                                                                                                        3174 Porter Drive
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                     PF-0348 US
                                                                                                                                                                                                          Version
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Best Local Similarity 34.4
58; Conservative
                                                                                                  FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                PRIOR APPLICATION NUMBER: PCT/US00/04414 PRIOR FILING DATE: 2000-02-22
                                                                                                                                                 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                               APPLICATION NUMBER: US 60/143,048 FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698 FILING DATE: 1999-07-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE 173
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                                                                                                                                                                                                                                Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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Botstein, David
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Gerritsen, Mary E.
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Eaton, Dan L.
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; Pred. No. 1.2e-19
36; Mismatches 7
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; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
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SEQ ID NO 34
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Best Local Similarity
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APPLICATION NUMBER: PCT/US99/23089
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175 DSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQK
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                                      DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE
                                                                            KRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQ 174
                                                                                                              SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP---GVPKVLVWVTDGGSS 117
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                                                                                                                                                                                                                                   Score 251.5; DB Pred. No. 2e-19; 6; Mismatches
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US-09-905-125A-34 GENERAL Patent No. PPLICANT 34, ... No. 666437, INFORMATION: Application US/09905125P Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. dao, Wei-Qiang Gerber, Hanspeter Ferrara, Napoleone Filvaroff, Ellen Desnoyers, Luc Eaton, Dan L. Botstein, David Ashkenazi, Avi

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RESULT 8
US-09-902-775A-34
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
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Best Local S
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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TYPE: PRT
ORGANISM: Homo sapiens
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IOR APPLICATION NUMBER: US 60/146,222
IOR APPLICATION NUMBER: US 60/146,222
IOR APPLICATION NUMBER: PCT/US99/20594
IOR APPLICATION NUMBER: PCT/US99/20594
IOR APPLICATION NUMBER: PCT/US99/20944
IOR FILING DATE: 1999-09-13
IOR APPLICATION NUMBER: PCT/US99/21090
IOR APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/23089
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FILING DATE: 1999-12-20
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T: Wood, William, I.
INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                      h 27.5%; Score 251.5; DB 2;
Similarity 32.2%; Pred. No. 2e-19;
58; Conservative 36; Mismatches 79;
                                                                                                                       DSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQK
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US-09-902-775A-34
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
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GENERAL INFORMATION:
                                                                           NUMBER OF SEQ
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 2000-01-05
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               TYPE: PRT
ORGANISM: Homo sapiens
                                                          ENGTH: 915
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Grimaldi, Christopher
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Gerritsen, Mary E.
Goddard, A.
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Best Local
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APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/143,048 FILING DATE: 1999-07-07
                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                             APPLICATION NUMBER: US 60/146,222 FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US00/04414
                                   APPLICATION NUMBER: PCT/US99/23089
                                                    FILING DATE: 1999-09-15
                                                                      APPLICATION NUMBER: PCT/US99/21547
                                                                                       FILING DATE:
                                                                                                        APPLICATION NUMBER: PCT/US99/21090
                                                                                                                          FILING DATE:
                                                                                                                                           APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                            FILING DATE: 1999-09-08
                                                                                                                                                                             APPLICATION NUMBER: PCT/US99/20594
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                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/906,700
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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Eaton, Dan L.
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Mather, Jennie P.
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Filvaroff, Ellen
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Botstein, David
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NUMBER: PCT/US99/28214
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Pred. No. 2e-19;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-34
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SEQ ID NO 34
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                                                    APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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Ashkenazi, Avi
Botstein, David
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Stewart, Timothy A.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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RESULT 11
US-09-904-920A-34
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; ORGANISM: Homo
US-09-903-603A-34
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Patent No. 6806352
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Best Local Similarity
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APPLICANT:
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
LENGTH: 915
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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APPLICATION NUMBER: PCT/US99/28565
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FILING DATE: 1999-11-30
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APPLICATION NUMBER:
FILING DATE: 1999-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                  Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                       Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                 KRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTF
                     Fong, buckers
Gao, Wei-Qiang
                                                              Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary E
                 Gerber, Hanspeter
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JUMBER: US
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PRIOR FILING DATE: 2000-01-
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
LENGTH: 915
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                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-904-920A-34
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Best Local Similarity
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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APPLICATION NUMBER: PCT/US99/28564
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                                      KRKSEVERÁVKRMRHLSTGTMTGLÁIQYÁLNIAFSEAEGARPLRENVPRVIMIVTDGRPQ 174
                                                                                                            RADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGFDVTRVGLLQYGSTVKNEFSLKTF 114
DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE
                                                                       SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP---GVPKVLVWVTDGGSS 117
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Mather, Jennie P.
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Kljavin, Ivar J.
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Grimaldi, Christopher
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                                                                                                                                                                                   27.5%; ilarity 32.2%; Conservative 3
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                                                                                                                                                                                   Score 251.5; DB 2;
Pred. No. 2e-19;
6; Mismatches 79;
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RESULT 12
US-09-909-064-34
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: US 60/143,048
TITTED DATE: 1999-07-07
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                                                                        APPLICATION NUMBER: PCT/US99/30911
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                                                                                                                             FILING DATE:
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                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/28564
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US99/20944
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                                                       FILING DATE:
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                                                                                                          APPLICATION NUMBER: PCT/US99/30095
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                                    APPLICATION NUMBER: PCT/US99/30999
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Eaton, Dan L.
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NUMBER: PCT/US00/00219
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Kenneth, J.
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Best Local S
Matches 58
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                                                                                                                                                               TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT FILING DATE: 2001-07-13
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1099-07-07
PRIOR FILING DATE: 1099-07-07
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TYPE: PRT
ORGANISM:
                                   PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR APPLICATION NUMBER: US 60/145,698
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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                                                                                                                                                                                                                                                                                                                                    Williams, P. M. Wood, William,
                                                                                                                                                                                                                                                                                                                                                                                               Stewart,
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Botstein, David
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Eaton, Dan L.
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Mather, Jennie P.
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                                                                                                                                                                                                                                                                                                                                                          P. Mickey
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LENGTH: 915
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Best Local s
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                                  APPLICANT:
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ORGANISM: Homo sapiens
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US00/00219
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APPLICATION NUMBER: PCT/US99/30999
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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58; Conservative
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP---GVPKVLVWVTDGGSS
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              Roy, Margaret
Stewart, Timot
Tumas, Daniel
                                                                                Kljavin, Iva.
Mather, Jennie P.
                                                                                                          Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Williams,
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Grimaldi, Christopher
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Gerritsen, Mary E.
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                                                           Paoni, Nicholas F.
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                           Margaret Ann
art, Timothy A.
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APPLICANT:

Desnoyers,

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RESULT 15
US-09-906-646-34
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Sequence 34, Application US/09906646
Patent No. 6852848
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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CURRENT FILING DATE: 2001-07-16
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1999-11-29
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ORGANISM: Homo
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Pred. No. 2e-19;
6; Mismatches
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                                                                                                                                              ; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-646-34
                                                              Query Match 27.5%;
Best Local Similarity 32.2%;
Matches 58; Conservative 36
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE:
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 423
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FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/20594
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Gao, Wei-Qiang
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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SUMMARIES

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A;Molecule type: mRNA, A;Molecule type: mRNA, A;Residues: 2960-2976, F',2978-3074, 'AG' <GOR3> A;Residues: 2960-2976, F',2978-3074, 'AG' <GOR3> A;Cross-references: UNIPARC:UPIO0001712F4; EMBL.M17375; NID:g211649; PIDN:AAA48718.1; PA;Note: this sequence has been revised in reference A34485 R;Koch, M.; Bernasconi, C.; Chiquet, M. R;Koch, M.; Bernasconi, C.; Chiquet, M. Biochem. 207, 847-856, 1992 Eur. J. Biochem. 207, 847-856, 1992 A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of A;Reference number: S23814; MUID:92362621; PMID:1323460

A;Molecule type: protein
A;Residues: 'X',1335, 1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
A;Cross-references: UNIPARC:UPI0000173C41; UNIPARC:UPI0000173C42; UNIPARC:UPI0000173C43
R;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin A;Reference number: S22254; MUID:88087065; PMID:3121603

A;Accession: S22254

A;Molecule type: protein

A; Accession: S23814

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tenascin Y precurs cell surface glyco	fibronectin precur integrin beta-4 ch	fibronectin - bovi tenascin precursor	protein-tyrosine-p fibronectin - chic	von Willebrand tac VLA-2 protein homo	fibronectin precur	tenascin-X - bovin cytotactin - chick	integrin alpha 2 s	tenascin-X precurs	lymphocyte fuction

ALIGNMENTS

RESULT 1 A40020 collagen alpha 1(XII) chain precursor - chicken
C;Dectes: Galle Balle Villeren, C. Dep-1999 #text change 09-Jul-2004 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004 :C;Accession: A40020; A34485; B34485; A28037; S23814; S22554; S28811 R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Oba J. Cell Biol. 115. 209-221, 1991
A; Title: The complete primary structure of type XII collagen shows a chimeric molecule
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site A;Reference number: A40020; MUID:92011862; PMID:1918137
A;Accession: A40020
A; Molecule type: mRNA A; Residues: 1-3124 < YAM>
A;Cross-references: UNIPROT:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810; PIDN
A;Note: in the authors' translation residues 1216-1219 are shown after residue 1: R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A;Title: Type XII collagen. A large multidomain molecule with partial nomology to type A;Reference number: A34485; MUID:90062079; PMID:2584192 A.Accession: A14485
A; Molecule type: mRNA
A; Restudes: 435-2736; A; 2700-2007; F; 2004-2976; F; 2576-3424; CONF A; Cross-references: UNIPARC: UPI0000171233; EMBL: J05137; NID: 9211284; PIDN: AAA48635: 1;
A;Accession: B34485 A:Molecule type: protein
A; Residues: 2772-2792; 2846-2873 < GOR2>
A;Cross-references: UNIPARC:UPI0000173C3F; UNIPARC:UPI0000173C40 R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA (A:Reference number: A28037; MUID:87317590; PMID:3476925
A;Accession: A28037
A. MOLOCILLO TYPOS MRNA

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F;2438-2440/Region: c
F;2509-2750/Domain: I
F;2751-2902/Domain: c
F;2899-2901/Region: c
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F;437-601/Domain: von Willebrand factor type A repeat homology
F;437-601/Domain: IIIC #status predicted <IIIC>
F;630-711/Domain: fibronectin type III repeat homology FN3C>
F;731-802/Domain: fibronectin type III repeat homology FN3D>
F;812-895/Domain: fibronectin type III repeat homology FN3F>
F;905-966/Domain: fibronectin type III repeat homology FN3F>
F;905-966/Domain: fibronectin type III repeat homology FN3F>
F;905-1076/Domain: fibronectin type III repeat homology FN3F>
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F;24-105/Domain: fibronectin type III repeat homology <FN3A>
F;137-301/Domain: von Willebrand factor type A repeat homology
F;332-425/Domain: IIIB #status predicted <IIIB>
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F;2325-2490/Domain:
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F;2119-2199/Domain:
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A; Residues: 1-24,1189-1257,'S',1259-1263,'B',1265-1280
A;Cross-references: UNIPARC:UPI0000173C46; EMBL:X67327
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A;Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45
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Biophys. Acta 1171, 97-98, 1992
Biophys. Acta 1171, 97-98, 1992
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                                                                                                                                                                                                                                                                                 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI-
                                                                                                                                                                                                                                                                                                                                                                                           NRVKDIIQAINTFPYRGGSTNTGKAMTYVREKVFVTSKGSRPNVPRVMILITDGKSSDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KADVVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPRKVQISLVQYSRDPHMBFSLNRY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                              SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV : : | : | : | : | : | : | | | | | |
LRIEQELAAIRKKSYVPAKNMVFSDVTSDSFKVSWSAAGSEEKSYLIKYKV--AIGGDEF
                                                                                                -----LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAAR 257
                                                                                                                                                                                                KEPAIKLRDADVEIFAVGVKDAVRTELEAIASPPAETHVYTVEDFDAFQRISFELTQSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in: fibromectin type III repeat homology <FN3I>
in: fibromectin type III repeat homology <FN3J>
in: fibromectin type III repeat homology <FN3J>
in: fibromectin type III repeat homology <FN3L>
in: fibromectin type III repeat homology <FN3L>
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in: fibromectin type III repeat homology <FN3P>
in: toromectin type III repeat homology <FN3P>
in: toromectin type III repeat homology <FN3P>
in: toromectin type III repeat homology <FN3P>
in: von Willebrand factor type A repeat homology <WN3P>
in: toromectin type III repeat homology <WN3P>
in: collagenous COL2 #status predicted <COL2>
on: collagenous COL2 #status predicted <COL2>
on: collagenous COL2 #status predicted <COL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gnal sequence #status predicted <SIG>
: collagen alpha 1(XII) chain #status predicted <MAT>
: dollagen alpha 1(XII) chain short splice form
IIIA #status predicted <IIIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.3%;
31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2887/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 437.5; DB 2;
Pred. No. 1.6e-22;
6; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2899/3; 2922/1; 2985/1; 3008/1; 3065/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  common
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  < VWA1 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              < VWA3 >
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(Pro)
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Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A;Title: Molecular cloning and characterization of type VII collagen cDNA
A;Reference number: PH0844; MUID:92231902; PMID:1567409
A;Rocession: PH0844
A;Molecular Collagen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Restdues: 'EFR', 372-517,'DV', 520-540,'W', 542-1255 < RES>
A; CROSS-references: UNIPARC:UPI000016B3AC; GB:S51236; NID:g262308; PIDN:AAB24637.1;
A; CROSS-references: UNIPARC:UPI000016B3AC; GB:S51236; N.P.; Glanville, R.W.; Burgeson,
R; Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson,
J. Biol. Chem. 264, 3822-3826, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J., J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot A;Reference number: I56328, MUID:93107742; PMID:1469284
A;Accession: I56328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, Proc. Natl. Acad. Sci. U.S.A. 88, 631-6335, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the A;Reference number: S16316; MUID:91334380; PMID:1871109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA, A;Molecule type: mRNA, A;Polecule type: mRNA, NID:g453698; PIDN: A;Experimental source: keratinocyte
A;Experimental source: keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-C;Accession: A54849; PH0844; SIS16; I56328; A30226; I84686 R;Christiano, A.M.; Greenspan, D.S.; Luet, S.; Uitto, J. Biol. Chem. 269, 20256-20262, 1994 Ph. Title: Cloning of human type VII collagen. Complete primary sequence A;Reference number: A54849; MUID:94327588; PMID:8051117 A;Accession: A54849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen alpha 1(VII) chain precursor - N;Alternate names: procollagen alpha 1(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
A54849
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                                                                       Hum. Mol. Genet. 2, 273-278, 1993
A; Title: The carboxyl-terminal half of type
A; Reference number: I48103; MUID:93271985; I
                                                                                                                                                                                                  A;Molecule type: protein
A;Molecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 815-892, E',894-1439 <PAR>
A;Cross-references: Unitaric: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Baue:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-2944 <CHR>
A;Cross-references: UNIPROT:Q02388; UNIPARC:UPI000017A138; GB:L02870; NID:g987124;
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                                                                                                                                                                                  A;Note: two reported peptides R;Greenspan, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A;Reference number: A30296; MUID:89139437; PMID:2537292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S16316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation
A;Status: preliminary; translated from
                                       A; Accession: I84686
                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVSVPASSTSSVLTNLLPETTYAVSVIAE-----YEDGDGPPLDGEETTLEVKGA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRNLRITDETTDSFIVGWTPAPGN--VLRYRLVYRPLTGGERRQVTVSANERSTTLRNLI 782
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   GB/EMBL/DDBC
                                                                           e VII collagen,
PMID:8499916
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                                                                                                                   including
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                                                                                                                       the non-collagenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the alpha1(VII
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PIDN:B

Mat

PID R.E

prot

PIDN:

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A;Cross-references: GDB:128750;
A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene ca
A;Note: there are 118 introns
C;Complex: type VII collagen is
C;Complex: type VII collagen is
C;Function:
A;Description: structural compo
C;Keywords: colled coll; extrac
F;1-16/Domain: signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1170-1172/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cysteine/proline-rich
F;1254-2783/Region: cysteine/proline-rich
F;1254-2783/Region: cill attachment (R-G-D) motif
F;1334-1336/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
F;25784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;337,786,1199/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;2167,2176,2185,2185,2664,2667,2673/Modified site: 4-hydroxypyroline (Pro) #s
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;36-201/Domain: von Willebrand factor type A repeat homology <VWAl>
F;231-318/Domain: fibronectin type III repeat homology <FN1>
F;237-413/Domain: fibronectin type III repeat homology <FN2>
F;414-502/Domain: fibronectin type III repeat homology <FN3>
F;508-593/Domain: fibronectin type III repeat homology <FN3>
F;508-593/Domain: fibronectin type III repeat homology <FN4>
F;508-693/Domain: fibronectin type III repeat homology <FN5>
F;686-771/Domain: fibronectin type III repeat homology <FN6>
F;706-862/Domain: fibronectin type III repeat homology <FN9>
F;864-952/Domain: fibronectin type III repeat homology <FN9>
F;864-952/Domain: fibronectin type III repeat homology <FN9>
F;864-952/Domain: fibronectin type III repeat homology <FN9>
F;8052-1219/Domain: von Willebrand factor type A repeat homology <VWA
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A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser A;Reference number: A55255; MUID:94224777; PMID:8170945
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Matches 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: GDB:COL7A1; EBR1; EBD1; EB
;Cross-references: GDB:128750; OMIM:120120
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GLDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPALGS
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                                                                                           RDLVLSEPSSQSLRVQWTAASGPVTGYKVQYTPLTGLGQPLPSERQEVNVPAGETSVRLR
                                                                                                                                                    QQLHATEITSSGFRLAWPPLLTADSGYYV--LELVPSAQPGAARRQQ--LPGNATDWIWA
                                                                                                                                                                                                                                                                                                                                       TGAAILHVADHVFLPQL-ARPGVPKVCILITDGKSQDLVDTAAQRLKGQGVKLFAVGIKN 177
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F;29-185/Product: collagen alpha 1(XIV) chain, short form #status predicted F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;352-433/Domain: fibronectin type III repeat homology <FN3C>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3E>
F;623-707/Domain: fibronectin type III repeat homology <FN3F>
F;623-707/Domain: fibronectin type III repeat homology <FN3F>
F;932-914/Domain: fibronectin type III repeat homology <FN3H>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
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A;Title: Complete primary structure of chicken collagen
A;Reference number: S31211; MUID:93185668; PMID:8444186
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A; Residues: 1-1857 < W
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117; Conserv
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EAQRVEVPAGRNCTTLQ--GLAPGTAYLVTVTAAFRSGRESALSAKACT
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                                                                                              PMASDLKLYDVSHS---SMRAKWN---GVAGATGYMILYAPLTEGL
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146 210 98

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glycoprotein;

region

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F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-188/Product: collagen alpha I(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3B>
F;442-527/Domain: fibronectin type III repeat homology <FN3B>
F;441-823/Domain: fibronectin type III repeat homology <FN3B>
F;441-823/Domain: fibronectin type III repeat homology <FN3B>
F;432-914/Domain: fibronectin type III repeat homology <FN3B-
F;832-914/Domain: fibronectin type III repeat homology <FN3B-
F;832-914/Domain: fibronectin type III repeat homology <FN3B-
F;822-109/Domain: fibronectin type III repeat homology <FN3B-
F;822-109/Domain: fibronectin type III repeat homology <FN3B-
F;832-914/Domain: fibronectin type III repeat homology <FN3B-
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A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793
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A;Residues: 1-1888 <TRU>
A;Cross-references: UNIPAOT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:g288872; R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1040-1205/Domain: von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;
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                                                                                                 EAQRVEVPAGRNCTTLQ--GLAPGTAYLVTVTAAFRSGRESALSAKACT 394
                                                                                                                                                                                                                         VRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGG-
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                                   AADEKEIKIGEASTELELDGLLPNTEYTVYVAMFGEEASDPLTGQETT 532
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                                                                                                                                                                                                                                                                                         --PTRGGQPEEVVVDGSSSTAVLKNLMSLTEYQIAVFAIYSNAASEGLRGTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ELRGSILDAM-RPQQLHATEITSSGFRLAWPPLLTADSG-----
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                                                                                                                                                              PMASDLKLYDVSHS---SMRAKWN---GVAGATGYMILYAPLTEGL
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A;Residues: 1472-1659 <GOR1>
A;Cross-references: UNIPARC:UPI0000173C49
A;Accession: S20833
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A;Title: Cloning of a cDNA for a new member of the class A;Reference number: S17035, MUID:92037585, PMID:1935930 A;Accession: S17035
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A;Title: Type XIV collagen is a variant of
A;Reference number: S22916; MUID:92339443;
A;Accession: S22916
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A; Residues: 1472-1660 < APT>
A; Cross-references: UNIPARC: UPI00000006A2;
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A,Note: sequence inconsistent with the nucleotide translation
A,Note: sequence extracted from NCBI backbone (NCBIN:133364, IR,Apte, S.S.
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A; Residues: 1551-1570; 1593-1599; 1639-1667 < GOR2>
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PFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGG
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                                                                                                                                                                                                                            64;
                                                                                                                                                                                                        Pred. No. 5.10
4; Mismatches
                                                                                                                                                                                                                                                   Score 369.5; DB z
Pred. No. 5.1e-18;
                                                                                                                                                                                                                                                                                                                                                       domain COL1 #status
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                                                                                                                                                                                                                                                                                   DB 2;
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F;40-204/Domain: von Willebrand factor type A repeat homology <PWA1>
F;236-401/Domain: fibronectin type III repeat homology <PW3A>
F;326-409/Domain: fibronectin type III repeat homology <PW3A>
F;418-498/Domain: fibronectin type III repeat homology <PW3C>
F;507-591/Domain: fibronectin type III repeat homology <PW3C>
F;507-591/Domain: fibronectin type III repeat homology <PW3D>
F;625-707/Domain: fibronectin type III repeat homology <PW3E>
F;716-998/Domain: fibronectin type III repeat homology <PW3F>
F;806-893/Domain: fibronectin type III repeat homology <PW3F>
F;806-893/Domain: non-collagenous NC4 #status predicted <NC4>
F;1111-1352/Domain: non-collagenous NC4 #status predicted <NC2>
F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F;1511-1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancullation of the control of the con
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A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439
A;Cross-references: UNIFARC:UPI0000173C48
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                                                             Type XIV collagen is encoded by alternative transcripts with distinct 5'
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R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele
A;Reference number: I51027; MUID:95246925; PMID:7729585
A;Accession: I51027
A;Status: preliminary.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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Pred. No. 7.2e-12;
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grins, Von Willebrand factor, compleme A;Reference number: A33809; MUID:89255 A;Accession: A33809 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-493 <KIS> A;Cross-references: UNIPROT:P05099; UN
                                                                                                                                                     cartilage matrix protein precursor - chicken
(;Species: Gallus gallus (chicken)
(;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
(;Accession: A33809; A26364
R;Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimber
J. Biol. Chem. 264, 8126-8134, 1989
A;Title: Structure of the gene for cartilage matrix protein, a modular proteins, Von Willebrand factor, complement factors B and C2, and epidermal gr
A;Reference number: A33809; MUID:89255246; PMID:2542265
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F;165-246/Domain: fibronectin type III repeat homology <FN3
F;255-338/Domain: fibronectin type III repeat homology <FN3
F;347-427/Domain: fibronectin type III repeat homology <FN3
F;347-632/Domain: fibronectin type III repeat homology <FN3
F;447-632/Domain: fibronectin type III repeat homology <FN3
F;547-632/Domain: fibronectin type III repeat homology <FN3
F;547-733/Domain: fibronectin type III repeat homology <FN3
F;641-723/Domain: fibronectin type III repeat homology <FN3
F;641-733/Domain: fibronectin type III repeat homology <FN3
F;741-818/Domain: fibronectin type III repeat homology <FN3
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C; Date: 30-Jun-1992 #sequence
C; Accession: A40970
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A; Residues: 1-843 < JUS>
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25.7%;
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UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347;

GB:X12

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RESULT 10
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A; Residues: 78-493 <ARC>
A; Residues: 78-693 <ARC>
A; Cross-references: UNIPARC: UPI000004FIEE; GB: M14792; NID: 9211545; PIDN: AAA48695.1;
C; Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A
F; 37-204/Domain: von Willebrand factor type A repeat homology <VWA1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cartilage matrix protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66522
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A;Title: Structural features of cartilage matrix protein deduced from A;Reference number: A26364; MUID:87092429; PMID:3025875
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Best Local S
Matches 60
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Best Local
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;270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
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66; Conserv
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                                                                                                IVVTDGRPQDSVRDVSERARASGIELFAIGLGRVDKATLRQIASEPQDEHVDYVE
                                                                                                                                             VWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVD 194
                                                                                                                                                                                            KPEFPLRAHGSKASLLQAVRRIQPLSTGTMTGLALQFAITKALSDAEGGRARSPDISKVV
                                                                                                                                                                                                                                         YTEFFFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGAR----PGVPKVL
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Pred. No. 4e-10;
2; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 243.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    No. 9.3e-10;
smatches 75;
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A;Introns: 30/1; 236/1; 437/1; 638/1; 838/1

C;Superfamily: collagen VI

C;Superfamily: collagen VI

C;Keywords: alternative splicing; cell binding; coiled coil; connective tissue F;1-25/Domain: signal sequence #status predicted <NGS-F;26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>F;26-2042/Domain: non-collagenous #status predicted <NNCS-F;26-2042/Domain: von Willebrand factor type A repeat homology <VW01>F;36-202/Domain: von Willebrand factor type A repeat homology <VW02>F;442-607/Domain: von Willebrand factor type A repeat homology <VW04>F;442-807/Domain: von Willebrand factor type A repeat homology <VW05>F;1837-1400/Domain: von Willebrand factor type A repeat homology <VW05>F;1033-1197/Domain: von Willebrand factor type A repeat homology <VW07>F;1237-1400/Domain: von Willebrand factor type A repeat homology <VW07>F;1839-1804/Domain: von Willebrand factor type A repeat homology <VW09>F;1838-2010/Domain: collagenous #status predicted <COL>F;2043-2378/Domain: collagenous #status predicted <COL>F;2045-2577/Domain: von Willebrand factor type A repeat homology <VW10>F;2863-2806/Domain: von Willebrand factor type A repeat homology <VW10>F;2863-2806/Domain: von Willebrand factor type A repeat homology <VW11>F;2863-2806/Domain: von Willebrand factor type A repeat homology <VW11>F;2863-3039/Domain: fibrongetin type A repeat homology <VW12>F;2863-3039/Domain: platelet glycoprotein ID-like #status predicted <GPI>F;2863-3039/Domain: fibrongetin type B III repeat homology <VW13>Fibrongetin type B III repeat homology <VW13>Fibro
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J. Biol. Chem. 264, 20235-20239, 1989
A;Title: The carboxyl terminus of the chicken alpha3 chain.
A;Reference number: A32674; MUID:90062147; PMID:2584214
A;Accession: A32674
A;Molecule type: mRNA
A;Residues: 2151-2199;2792-3137 <B02>
A;Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI00001
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A3/797; A.R;Doliana, R.; Bonaldo, P.; Colombatti, A. R;Doliana, R.; Bonaldo, P.; Colombatti, A. J. Cell Biol. 111, 2197-2205, 1990
A;Title: Multiple forms of chicken alpha3(VI) collagen chain
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A;Title: Structural and functional features of the alpha3 chain in A;Reference number: A34270; MUID:90212613; PMID:2322559
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A;Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A;Cross-references: UNIPROT:P15989; UNIPARC:UPI0000173C31; UNIPARC:UPI0000173C32;
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A37797; A34270; A32674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;2954-3039/Domain: fibronectin type III repeat homology <FN3>F;3072-3122/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A37797; MUID:91035630; A;Accession: A37797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI0000173C38; GB:M24282
A;Note: the authors translated the codon TTC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 224-2871 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A34270
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 76
                                          117
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LVYAKEQLFAEASGAR--PGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGN 174
                                                                                                                    LYDVVKALDVGGNDFRFALVQFSGNPHTEFQLNTYPSNQDVLSHIANMPYMGGGSKTGKG
                                                                                                                                                                                                                                                                                                                                      LPWTA-LGLALSLRLALARSGAERGPPASAPR----GDLMFLLDSSASVSHYEFSRVREF
                                                                                                                                                                                          VGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLA 116
                                                                                                                                                                                                                                                                LPLAAILGLLLS---GFCSVGAQQ---QAAVRNVAVADIIFLVDSSWSIGKEHFQLVREF
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 239; DB 2
Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIPARC: UPI0000173C3A; GB:M24282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 3137;
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A; Reference number: A59140
A; Accession: A59140
A; Status: not compared with
A; Molecule type: mRNA
A; Residues: 1-3176 < CHU>
A; Cross-references: UNIPROT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:CRTM
A;Cross-references: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1;
C;Complex: homotrimer
C;Superfamily: cartilage matrix protein; EGF homolog
C;Keywords: glycoprotein; homotrimer
C;Keywords: glycoprotein; homotrimer
C;Keywords: glycoprotein; signal sequence #status predicted <SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh. J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix A;Reference number: A37979; MUID:91060588; PMID:2246248
A;Accession: A37979
A;Molecule type: DNA
A;Residues: 1-496 <JEN>
A;Cross-references: UNIPROT:P21941; UNIPARC:UPI000004F1ED; GB:J05667
A;Accession: B37979
A;Molecule type: mRNA
A;Cross-references: uniparc:UNIPROT:P21941; UNIPARC:UPI000004F1ED; GB:J05667
A;Accession: B37979
A;Molecule type: mRNA
A;Residues: 157-290; L1, 292-496 <JEZ>
A;Residues: 157-290; L1, 292-496 <JEZ>
                                                                                                                                                                                                                                                           collagen alpha 3(VI) chain precursor [validated] - N;Contains: collagen alpha 3(VI) chain, splice form C;Species: Homo sapiens (man) C;Date: 21-Nov-1993 #sequence revision 12-Nov-1999 C;Accession: A59140; S13679; $24465; A57083; $28776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cartilage matrix protein precursor - C;Species: Homo sapiens (man) C;Date: 12-Jul-1991 #sequence_revisio C;Accession: A37979; B37979
                                                                                                                                                                                                  submitted to GenBank,
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Best Local S
Matches 62
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;1-22/Domain: signal sequence #status predicted <SIG>
;23-496/Product: cartilage matrix protein #status predicted <MAT>
;23-496/Domain: von Willebrand factor type A repeat homology <VWA
;227-262/Domain: EGF homology <EGF>
;227-262/Domain: BGF homology <EGF>
                                                                                                                                                                                                                                       ;Molecule type: mRNA;Residues: 157-290,'L',292-496 <JE2>;Cross-references: UNIPARC:UPI000016A6E8; GB:M55683;
                                                                                           Status: not compared with conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273-437/Domain: von Willebrand factor type A repeat homology <VWA2>76,344/Binding site: carbohydrate (Asn) (covalent) #status predicte 221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004;
Accession: A37979; B37979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: cartilage matrix protein; EGF homology; von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQVGLVQYSSSVRQEFPLGRFHT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAKKAKDLGFKMFAVGVGNAVEDELREIASEPVAEHYFYTADFKTINQIGKKLQKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PMQELKDLGVTVFIVSTGRGNFLELSAAASAP-AEKHLHFVDVDDLHIIVQELRGSI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGELKEIASRPFDTHLFNLENFTALHGIVGDLVASVRTSMTPEQAGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLELSAAASAPAEKHL-HFVDVDDLHIIVQELRGSILDAMRPQQLHA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKDIKAAVRNMSYMEKGTMTGAALKYLIDNSFTVSSGARPGAQKVGIVFTDGRSQDYIND 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEYLIENHLTKAAGSRASEGVPQVIIVLTDGQSQDDVALPSSVLKSAHVNMIAVGVQDAV
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   UNIPROT: P12111;
                                                                                                                                                                                                     May
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Pred. No. 4.7e-09;
7; Mismatches 87
   UNIPARC: UPI0000126D4F;
                                                                                                      translation
                                                                                                                                                                                                                                                                                                                                                              form
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   GB:X52022; NID:g3127925;
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Bur. J. Biochem. 133, 39-46, 1983

A;Title: Further characterization of the three polypeptide chains of bovine and huma A;Reference number: S26506; MUID:83209648; PMID:6852033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 2038-2373 <CH4>
A;Residues: 2038-2373 <CH4>
A;Residues: 2038-2373 <CH4>
A;CORS-references: UNIDARC:UPI0000173C2E; GB:J04211; GB:M20778
A;Note: parts of this sequence were determined by protein sequencing
A;Note: parts of this sequence were determined by protein sequencing
A;Note: parts of this sequence were determined by protein sequencing
A;Note: parts of this sequence were determined by protein sequencing
A;Note: parts of this sequence were determined by protein sequencing
A;Title: Cloning and Chromosomal localization of human genes encoding
A;Reference number: A29848; MUID:88161046; PMID:3348212
                                                                                                                                                            A;Cross-references: UNIPARC:UPI0000173C2F
A;Note: this sequence cannot be reliably placed and probably
R;Mayer, U.; Poeschl, E.; Nischt, R.; Specks, U.; Pan, T.C.;
Eur. J. Biochem. 225, 573-580, 1994
A;Title: Recombinant expression and properties of the Kunitz-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Chu, M.L.; Zhang, R.Z.; Pan, T.; Ste
EMBO J. 9, 385-393, 1990
A;Title: Mosaic structure of globular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; I
J. Biol. Chem. 263, 18601-18606, 1988
A;Title: Amino acid sequence of the triple-helical domain
A;Reference number: A31952; MUID:89066644; PMID:3198591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA; protein
A;Residues: 2024-2046;2092-2156,'R';2203-2208,'X',2210-2211,'X',2213-2227;2228-2251;231
A;Cross-references: UNIPARC:UPI000016A705; UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 310-328 <ZAN>
A;Cross-references: UNIPARC:UPI0000173C28
                                  A; Molecule type: mRNA
A; Residues: 'MRAWIFFLLCLAGRALAA', 3102-3176
                                                                                                      A; Accession: S48709
                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 'SAIAGVAGVG'
                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 2092-2151 <WEI>
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A; Residues: 574-
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A;Accession: S13679
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      UNIPARC: UPI 0000173C3
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T.; Stokes, domains D.; Conway, D.; in the human type Kuo, ۲ H.J.; Glanville, collagen alpha-3 R.; cha Ma

MUID:90151612; PMID:1689238

A;Molecule type: mRNA A;Residues: 1-30,237-313,'CWW',318-322,'AR',326-1815,'FD',1818-1819,'ID' A;Cross-references: UNIFARC:UPI0000173C14; EMBL:X52022; NID:g3127925 ,1822-3176 SES

A;Residues: 574-585;965-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',150
1962,'X',1964-1965;2018-2037;2374-2410;2445-2459;2466-2469,'X',2471-2474;2504-2508,'X'
A;Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C17
C1C; UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C17
10000173C25; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C27
R,Zanussai, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A;Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain A;Reference number: S28776; MUID:93054780; PMID:1339440

A; McCourage mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZA2>
A; Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZA2>
A; Cross-references: UNIPARC: UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1; PID
A; Cross-references: UNIPARC: UPI0000173C28; PIDN:AAB24261.1; PIDN:AAB

type ۲ĭ γģ peptide

the mRNA portion of the sequence corresponds to rM.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; residues 2092-2157 Deutzmann, Timpl,

of human collagen type

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D.; Mann, K.; Deut

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three

human

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represents Chu, M.L.; the results fro

A;FILLE: Recombinant expression and properties of the Kunitz-type A;Reference number: \$48709; MUID:95045506; PMID:7525281 protease-inhibitor

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YAM>

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File25/Domain: signal sequence #status predicted <MSTS
File2-176/Product: collagen alpha 3(VI) chain #status predicted <AMTS
File2-176/Product: collagen alpha 3(VI) chain #status predicted <AMTS
File26-10/2077-176/Product: collagen alpha 3(VI) chain, splice form A9/NIO(-) #status pred
File26-10/2077-176/Product: collagen alpha 3(VI) chain, splice form A9/NIO(-) #status pred
File26-10/2077-176/Product: collagen alpha 3(VI) chain, splice form A9/NIO(-) #status pred
File26-10/2077-176/Product: collagen alpha 3(VI) chain, splice form A9/NIO(-) #status pred
File26-10/2077-176/Domain: von Willebrand factor type A repeat homology <WW03>
File27-1191/Domain: von Willebrand factor type A repeat homology <WW05>
File37-1191/Domain: von Willebrand factor type A repeat homology <WW05>
File37-1191/Domain: von Willebrand factor type A repeat homology <WW05>
File37-1191/Domain: von Willebrand factor type A repeat homology <WW05>
File37-1191/Domain: von Willebrand factor type A repeat homology <WW05>
File36-1199/Domain: von Willebrand factor type A repeat homology <WW05>
File37-1294/Domain: von Willebrand factor type A repeat homology <WW05>
File37-1294/Domain: von Willebrand factor type A repeat homology <WW05>
File37-1295/Region: cell attachment (R-G-D) motif
File37-1295/Region: cell cell ce
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A;Cross-references: GDB:119066; OMIM:120250
A;Cross-references: GDB:119066; OMIM:120250
A;Cross-references: GDB:119066; OMIM:120250
A;Cross-references: GDB:119066; OMIM:120250
C;Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA)
Sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
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A;Reference number: A52812; PDB:IKNT
A;Contents: annotation; X-ray crystallography, 1.6 angstroms, residues 3106-3160
A;Note: engineered sequence expressed in Saccharomyces cerevisiae strain mt-663
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit sines are 5-hydroxylated and subsequently O-glycosylated.
C;Comment: The fibronectin type III repeat homology domain may be released during proce-
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Best Local
                                                          211 DAMRPQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQLPGNATDWIW
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                                                                                                                     ALPSAELKSADVNVFAIGVEDADEGALKEIASEPLNMHMFNLENFTSLHDIVGNLVSCVH
                                                                                                                                                                                    GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL-HFVDVDDLHIIVQELRGSIL
                                                                                                                                                                                                                                                                                                         GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGAR---PGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                                                                                                                                                           DIIFLVDSSWTIGEEHFOLVREFLYDVVKSLAVGENDFHFALVOFNGNPHTEFLLNTYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                         DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
SSVSPERAGDTETLKD--
                                                                                                                                                                                                                                                  KQEVLSHISNMSYIGGTNQTGKGLEYIMQSHLTKAAGSRAGDGVPQVIVVLTDGHSKDGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 225.5; DB 2; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 143;
-ITAQDSADIIFLID--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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A; Accession: T46488
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A; Residues: 1-741 < AAA>
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Best Local
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57
                                                                                                                                                      Similarity
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DIVIVLDGSNSI--YPWESVTAFLNSLLRNMDIGPQQTQVGIVQYGQTVVHEFYLNTYST
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                                                                                                                            Conservative
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R;Kern, A.; Briesewitz, R.; Bank, I.; Marcantonio, E.E.
J. Biol. Chem. 269, 2281-22816, 194
A;Title: The role of the I domain in ligand binding of the human integrin alpha-lbeta-1
A;Reference number: A55348; MUID:94357930; PMID:7521332
A;Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Gallus gallus (cnicken)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55348
C;Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein DKFZp434J065.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #te C;Accession: T46488
                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-272 <KER>
A;Residues: 1-272 <KER>
A;Cross-references: UNIPROT:O42094; UNIPARC:UPI000017A14E; GB:U10114
F;55-230/Domain: von Willebrand factor type A repeat homology <VWA2>
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A;Experimental source: adult testis; clone DKFZp434J065
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 AKDMKKAV-AHMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 PYGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGS
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34 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 93
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                                                                     9.7%; Score 209; DB 2; Length 272; 33.6%; Pred. No. 1.2e-07; ative 31; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.2%; Score 220; DB 2; 31.9%; Pred. No. 7.1e-08;
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GenCore version (c) 1993 - 2006

5.1.7 Biocceleration

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Title:
Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. "
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Q9H6J5_HUMAN
Q8VDVYK1_HUMAN
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SMART; SM00060; FN3; 2
SMART; SM00327, VWA; 1
PROSITE; PS50853; FN3;
PROSITE; PS50234; VWFF
                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
13-SEP-2005 (TrEMBLrel. 21, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Von Willebrand factor A domain-related protein (Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031410123 product:VON WILLEBRAND RELATED PROTEIN homolog).
Mammary tumor metastatized to lung. Tumor arose spontaneously; MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
Muroidea; Muridae; N
                                                                                                                                                                                          STRAIN=Czech II, and TISSUE=Colon, and
                                                                                                                                                                                                                                                NUCLEOTIDE
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PS50853; FN3; 2.
PS50234; VWFA; 1
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                                                                                                                                                                                                                                              SEQUENCE.
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                                                                                                                                                                                                                                                                                                                   Murinae;
                                                                                                                                                                                                                                                                                                                                         Chordata; Craniat.
Euarchontoglires;
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93.9%;
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Pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euto
Oglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D9FBDE9C0A4DEBDF CRC64;
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-lock. T and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RX MEDLINE-257BL/G; TISSUE=Ovary and uterus;
RX MEDLINE-2108560; pubMed=11217851; DOI=10.1038/35055500;
RX MEDLINE-2108560; pubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Sibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Mateuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Mateuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schreiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schreiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Bromstein M.J., Bult C., Fletcher C., Fujita M., Garriboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

***Tanaka Y., Kamaji H., Kohtsuki S.,
***Tanaka Y., Kawaji H., Kohtsuki S.,
***Tanaka Y., Storch K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
***Tanaka Y., Kohtsuki S.,
***Tanaka Y., Kawaji H., Kohtsuki S.,
***Tanak
                                                                                                                                                   NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/60; TISSUE=Ovary and uterus;

STRAIN=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Y., Maramatsu M., Hayashizaki Y.;

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cD!"

"Normalization and subtraction of rapid discovery of the contraction of cap-trapper-selected cD!"

"Normalization and subtraction of cap-trapper-selected cD!"
NUCLEOTIDE SEQUENCE.
STRAIN=C57EL/6J; TISSUE=Ovary and uterus;
MEDLINE=20530911; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Ovary
The FANTOM Consortium,
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Hayashizaki Y.;
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; DOI=10.1016/S0076-6879(99)03004-9;
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A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

A Hayashida K., Hayatsu N., Hiranoto K., Hiraoka T., Kasukawa T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sakabashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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SWART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50683; FN3; 2.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44737 MW;
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MEDLINE=22057805; PubMed=12062410; DOI=10.1016/S0014-5793(02)02579-6; Fitzgerald J., Ting S.T., Bateman J.F.;

"WARP a new member of the von Willebrand factor A-domain superfamily of extracellular matrix proteins.";
FEBS Lett. 517:61-66(2002).

EMBL; AY030094; AAX38350.1; -; mRNA.
HSSP; P18614; 1MHP.
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Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
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MGI; MGI:2179729; Vwa1.
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A Hayashizaki Y.,
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4932416All product:VON WILLEBRAND FACTOR A-RELATED
PROTEIN homolog.
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Q8C0Q7;
Q8C0Q7;
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TIS
MEDLINE=20530913; Pu
                                                                                                                          Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs t prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Testis; The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUE=Testis;
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Mammalia; Eutheria;
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TISSUE=Testis; pubMed=11076861;
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   DOI=10.1101/gr.152600;
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RC STRAIN=57BL/6J; TISSUB=Testis;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Hothi S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hoti F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

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RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

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RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, AK030019; BAC26739.1; -; mRNA.
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PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44681 MW;
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MGI; MGI:2179729; Vwa1.
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AS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

AR Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AR Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AR Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

AR Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AR Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AR Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

AR Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

AR Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

AR Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AR Brownstein M.J., Woln T.B., Toshiyuki S., Carninci P., Prange C.,

AR ARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

AR Hillian D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

AR Hillian D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

AR Hillian D.K., Worley K.C., Shevchenko Y., Bouffard G.G.,

AR Hillian D.K., Touchman J.W., Green E.D., Dickson M.C.,

AR Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

AR Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

AR Schein J.E., Jones S.J.M., Marra M.A.;

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

AR Generation and initial analysis of more than 15,000 full-length human

AR Generation and initial analysis of more than 15,000 full-length human
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Von Willebrand factor A domain-related protein.
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PROSITE; PS50853; FN3; 2.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC081983, AAH81983.1; -; mRNA. InterPro; IPR003961; FN III. InterPro; IPR002035; VWF_A. Pfam; PF00041; En3; 2. Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00453; VWFADOMAIN SMART; SM00060; FN3; 2. SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=RGD1311476_predicted;
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                                                                                                                                                                                                            1 MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                   VAPLPLGTGALRASLVHVGSRPYTEFPFFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                          KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
                                                                                                                                                                    KEQLFAEEAGARLGVPKVLVWVTDGASSDSVGPPMQELKDLGVTIFIVSTGRGNLLELLA
                                                                                  VATMPFGPGALRASLVHVGSRPHTEFTFDQYSSGQAIQDAVRVAPQRMGDTNTGLALAYA
                                                                                                                                                                                                                                                                                                                                           415 AA;
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                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                         44832 MW;
                                                                                                                                                                                                                                                                          76.38;
                                                                                                                                                                                                                                                    ; Pred. No. 3.50
                                                                                                                                                                                                                                                                          Score 1643.5; DB 2; Pred. No. 3.5e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                           B3A0A0268DB06D4E CRC64;
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RESULT 6
Q7L5D7_HU
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                                                                                                                               ACC STREET REPORTED BY THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K.J., Sonaldo M.F., Casavant T.L., Scheet T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robas S.A., WcEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Robas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Smailus D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
The Common of the Common o
                          Query Match
Best Local Similarity
Matches
                                                                                                                     Pfam; PF00041; fn3; 2.

SMART; SM00060; FN3; 1.

PROSITE; PS50853; FN3; 2.

NON TER 1 1

SEQUENCE 281 AA; 29628 N
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13-SEP-2005 (
13-SEP-2005 (
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07 HUMAN PRELIMINARY;
Q7L5D7;
                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC003543; AAH03543.2; -; mRNA. InterPro; IPRO03961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=WARP;
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                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                      FISSUE=Pancreas;
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254;
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                                                                                                                               281 AA; 29628 MW;
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Conservative
                              60.1%;
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Last annotation updat
<u>°</u>
Score 1295.5;
Pred. No. 1.4e
0; Mismatches
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                                                                                                                               350CCE4590791BD4 CRC64;
                              No. 1.4e
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                              5; DB
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                                                                   281;
   27;
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RESULT 7
Q9H6J5 HUMAN
ID G9H6J5;
DT 01-MAR-2001 (7
DT 01-MAR-2001 (7
DT 01-MAR-2001 (7
DT 01-CT-2003 (7
DT 01-MAR-2001 (7
DR NUCLEOTIDE SEC
RA Watanabe K., #
RA Wat
RESULT 8
Q8VDV9 MOUSE F
ID Q8VDV9 MOUSE F
AC Q8VDV9;
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Best Local S
Matches 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Watanabe K., Kumdgai A., Itakura S.,
Watanabe K., Kumdgai A., Nishi T., Sh
Suzuki Y., Obayashi M., Nishi T., Sh
Nakamura Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/Ger
EMBL; AKO25868; BAB15264.1; -; mRNA.
HSSP; Q96KP7; 1FNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS50853; FN3; 2.
SEQUENCE 233 AA; 24473 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q96KP7; 1FNA.
Ensembl; ENSG00000179403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ22215.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                            366
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                 LAPGTAYLVTVTAAFRSGRESALSAKACTPDGPRPRPRPVPRAPTPGTASREP
                                                                                                                                                                                                    AGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQG
                                                                                                                                                                                                                                                                         LDPDTDYDVALVPESNVRLLRPQILRVRTR-----------
                                                                                                                                                                                                                                                                                                                            MRPQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQLPGNATDWIWAG
                                                                                                                                                                                                                                                                                                                                                  MRPQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQLPGNATDWIWAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAPGTAYLVTVTAAFRSGRESALSAKACTPDGPRPRPRPVPRAPTPGTASREP
                                                                                                                                                                                 AGPERIVI SHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQG
                                                                                                                                                                                                                                                     LDPDTDYDVALVPESNVRLLRPQTLRVRTRPGEAGPGASGPESGAGPAPTQLAALPAPEE
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                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                              49.1%;
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---~hi T., Shibahara T
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                    PRT;
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ibahara T., Tanaka
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005615; C:extracellular space; InterPro; IPR003961; FN_III. Pfam; PF00041; fn3; 2. SMART; SM00060; FN3; 2.
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Ensemb; ENSWUSG00000042116; Mus
MGI; MGI:2179729; 4932416A11Rik.
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Submitted (DEC-2001) to the
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                                                    CTPDGPRPRPRPVPRAPTPGTASREP
                  CTASGARTR --- APQSMRPEAGPREP
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                                                                                                                                                                                                                                                                                                           Conservative
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RC TISSUE-Manmary tumor metastatized to lung. Tumor arose spontaneously;

RM MEDLINE-22388257; pubMede12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Medin N.B., Bonaldo M.F., Gardanon R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Touchman J.W., Green E.D., Dickeon M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

"Torn" Medical T.S., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                    LDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPALGSA
                                                                                                                                                                                                                                                                                                                  AALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQGLAPGTAYLVTVTAAFRSGRESALSAKA
SALGYHVQLGPLQGGSLERVEVPAGQNSTTVQGLTPCTTYLVTVTAAFRSGRQRALSAKA
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Last annotation updat
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Pred. No. 1.2e-45;
7; Mismatches 35
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
RA Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Cruaud C., Duprat S., Brottier P., Cottanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Railis M., Volff JN., Guigo R., Zody M.C.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weisenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
T the early vertebrate proto-karyotype.";
Nature 431:946-957 (2004).
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Best Local S
Matches 146
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Q4SCD1;
13-SEP-2005 (TEMBLrel. 31.
13-SEP-2005 (TEMBLrel. 31.
13-SEP-2005 (TEMBLrel. 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope; Whitehead Institute Centre for Genome Submitted (FEB-2004) to the EMBL/GenBank/DDBJ dat -!- CAUTION: The sequence shown here is derived f EMBL/GenBank/DDBJ whole genome shotgun (WGS)
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Bukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sanutation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14659, whole genome sho
ORFNames=GSTENG00020556001;
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VTVTAAFRSGRESALSAKACTPDG
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                                                                                                                                                                                                                                                                     ARRQQL--PGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVI
                                                                                                                                                                                                                                                                                                                                                    ELIRAERLNVRDISTNSASLHWRPVLAGMRGYYEVRFAPLPTKVPGGGGENTGTSPSTGG
                                                                                                                                                                                                                                                                                                                                                                                                            DAMRPQQLHATEITSSGFRLAWPPLLTADSGYYVLELVP-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDVLFLLDSSGSVSSYEHSRMLAFLSELLQPFSLGEDQVRVGVLQVGTEPRLEFGFDAHA
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                                                                                               TESGATSVRLSWGP-LQPQTVRDYYIEYSALPRGELRTATVDRTQNSTLLRRLQPGTTYL
                                                                                                                                                        SHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQGLAPGTAYL
                                                                                                                                                                                                                          SQYQRLVQPAASSTAKLTGLKPDTTYTVTLIPESNEHTFNALTTTFTTKPEVLSPVVVTV
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55316 MW; C724FA399E0751FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute Centre for Genome Research; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
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Pred. No. 1.9e-38;
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P13944; Q04509;
01-JAN-1990 (Rel
                                                                                                                                            ul-NUV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Collagen alpha 1(XII) chain precursor (Fibrochimerin)
Name=COL12A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93042014; PubMed=1420368; DOI=10.1016/G
Trueb J., Trueb B.;
Trueb J., Trueb B.;
"The two splice variants of collagen XII share
Biochim. Biophys. Acta 1171:97-98(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to type J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=White leghorn;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MISSING Y. SANION OF TANAMAN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon M.K., Gerecke D.R., Olsen B.R.; "Type XII collagen: distinct extracellular matrix component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90062079; PubMed=2584192; Gordon M.K., Gerecke D.R., Dublet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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                                  Event=Alternative splicing; Named isoforms=2; Comment=The final tissue form of collagen XII may contain homotrimers of either isoform long or isoform Short or any combination of isoform Long and isoform Short. Only isoform Long is a proteoglycan. Isoform Long has more restricted expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
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XII collagen. A
                        is a proteoglycan. Isoform Long has mor in embryonic tissue than isoform Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloning.";
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; Galliformes; Phasianidae; Phasiani
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InterPro; IPR008160; Collagen.

InterPro; IPR0031961; FN III.

InterPro; IPR0031951; Laminin_G_TSP_N.

InterPro; IPR002035; VWF A.

InterPro; IPR002035; VWF A.

InterPro; IPR002035; VWF A.

Pfam; PF001991; Collagen; 4.

Pfam; PF000941; fn3; 17.

Pfam; PF000941; fn3; 18.

RPART; SM00205; VWA; 4.

R PRONTS; PR00453; VWFADOWAIN.

R SMART; SM00207; VWA; 4.

R SMART; SM00207; VWA; 4.

R PROSITE; PS50853; FN3; 18.

R PROSITE; PS50853; FN3; 18.

R PROSITE; PS50234; VWFA; 4.

Alternative splicing; Cell adhesion; Collagen;

W Alternative splicing; Extracellular matrix; Glyc's Allernative splicing; Extracellular matrix; Glyc's Allernative splicing; Extracellular matrix; Glyc's Allernative splicing; Repeat; Signal; Extractural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D00824; BAA00701.1; -; m
EMBL; X61024; CAA43358.1; -; m
EMBL; M17375; AAA48718.1; -; m
EMBL; J05137; AAA48635.1; -; m
EMBL; X67327; CAA47744.1; -; m
PIR; A40020; A40020.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s Swiss-Prot entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family. SIMILARITY: Contains 18 fibronectin type-III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P13944-2; Sequence=VSP_001148; TISOID SPECIFICITY: Type XII collagen is present in tendons, ligaments, perichondrium, and periosteum, all dense connective tissues containing type I collagen.

DOMAIN: This sequence defines five distinct domains, two triple-helical domains (COL1 and COL2) and three nontriple-helical domains (NC1, NC2, and NC3).

PTW: The triple-helical tail is stabilized by disulfide bonds at another.
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                                                                                         PGTAYLVTVTAAFRSGRESALSAKACTPDGPRPRPR
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                                                                                                                                                                                                                                         RQQLPGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHAR
                                                                                                                                                                                                                                                                                                                  -----LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAAR
                                                                                                                                                                                                                                                                                                                                                       KEPAIKLRDADVEIFAVGVKDAVRTELEAIASPPAETHVYTVEDFDAFQRISFELTQSVC
                                                                                                                                                                                                                                                                                                                                                                                                                               NRVKDIIQAINTFPYRGGSTNTGKAMTYVREKVFVTSKGSRPNVPRVMILITDGKSSDAF
                                                    PDTRYEVSVIAEYQSGPGNALNGYAKT-DEVRGNPR
                                                                                                                              PRNLRITDETTDSFIVGWTPAPGN
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                                                                                                                                                                 -VSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QP ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arg/Lys-rich (basic).
N-linked (GlcNAC...)
O-linked (Xyl...) ((
(Potential)...) ((
(Potential)...)
N-linked (GlcNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked ()
N-link
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 437.5; DB 1
Pred. No. 1.2e-20;
5; Mismatches 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     imperfection.
Nonhelical region (NC2).
Triple-helical region (COL1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nonhelical region (NC3).
Triple-helical region (COL2) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asp/Glu-rich (acidic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imperfections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibronectin type-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             094285AFE7F346CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Id=VSP_001148.
S (in Ref. 4).
S (in Ref. 2).
A (in Ref. 2).
(in Ref. 2).
F (in Ref. 2).
F (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elical region (NC1).
                                                                                                                              --VLRYRLVYRPLTGGERROVTVSANERSTTLRNLI
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Length

3124;

Indels

39;

Gaps

496 151

91

209 556 .) (Pote .)

(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).

(chondroitin sulfate)

(chondroitin sulfate

(Potential) (Potential) (chondroitin

sulfate)

(Potential).

(Potential)

with

---YEDGDGPPLDGEETTLEVKGA

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RESIDENTIFY ENGGOODOUILT79; Homo Bapiens.

RESIDENTIFY ENGGOODOUILT79; Homo Bapiens.

RESIDENTIFY ENGGOODOUILT79; Homo Bapiens.

RESIDENTIFY ENGGOODOUILT79; C:extracellular matrix (sensu Metazoa); IEA.

RESIDENTIFY ENGGOODOUILT ENGGOODOUILT ENGGOODOUITS; P:ecall adhesion; IEA.

RESIDENTIFY ENGOSITE; P:ecall adhesion; IEA.

RESIDENTIFY ENGOSITE; P:ecall adhesion; IEA.

RESIDENTIFY ENGOSITE; P:ecallular matrix; Repeat; Structural protein.

RESIDENTIFY ENGGOODOUILT ENGGOODOUITS; IEA.

RESIDENTIFY ENGOSITE; PSSOSIS; FN3; 18.

RESIDENTIFY ENGOSITE; PSSOSIS; FN3; 18.
                                                                                                                                                                                                                                                                 Query Match
Best Local Sim
Matches 120;
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Q5VYK2 HUMAN PRELIMINARY;
Q5VYK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL354664; CAH71309.1; -; Genomic_DNA.
EMBL; AL080250; CA119897.1; -; Genomic_DNA.
EMBL; AL080771; CA119807.1; -; Genomic_DNA.
EMBL; AL080250; CA171309.1; JOINED; Genomic_DNA.
EMBL; AL080771; CAH71309.1; JOINED; Genomic_DNA.
EMBL; AL086771; CA119897.1; JOINED; Genomic_DNA.
EMBL; AL080250; CA119807.1; JOINED; Genomic_DNA.
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01-FEB-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Collagen, type XII, alpha 1.
Name=COL12A1, ORFNames=RP1-23BD15.1-003;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tromans A
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                     558
                                                                                                                 498
                                                                                                                                                                                          438
 210
                                                                            152
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                     SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                              RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                      GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI-
                                       RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVEDFDAFQRISFELTQSIC
                                                                                                                 KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF
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                                                                                                                                                                                                                                                                   Conservative
 ---LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAAR
                                                                                                                                                                                                                                                                                     19.7%;
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                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                   Score 424; DB
Pred. No. 9.4e
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                       DB 2;
9.4e-20;
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                                                                                                                                                                                                                                                                                                    Length 2884;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                   Gaps
   257
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                                         617
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RESULT 12
Q5VYK1_HUM
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                                                                                                                                                                                                                                                          EMBL; AL354664; CAH71310.1; -; Genomic_DNA.

EMBL; AL080250; CAH19898.1; -; Genomic_DNA.

EMBL; AL096771; CAH19908.1; -; Genomic_DNA.

EMBL; AL096771; CAH71310.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH71310.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH71310.1; JOINED; Genomic_DNA.

EMBL; AL354664; CAH19908.1; JOINED; Genomic_DNA.

EMBL; AL080250; CAH19908.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH19908.1; JOINED; Genomic_DNA.
                                                                                                     InterPro; IPR002035; VWF A.
Pfam; PF01391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWA; 4.
PRINTS; PR00453; VWFADOMAIN.
SWART; SW00060; FN3; 18.
SWART; SW00210; TSPN; 1.
SWART; SW00210; TSPN; 1.
SWART; SW00327; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corby N.;
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequency
13-SEP-2005 (TrEMBLrel. 31, Last annotat
13-SEP-2005 (TrEMBLrel. 31, Last annotat
Collagen, type XII, alpha 1.
Collagen, type XII, alpha 1.
Name=COLI2A1; ORFWames=RP1-238D15.1-001;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; VWFA; 4.
Collagen; Extracellular ma
SEQUENCE 3063 AA; 33314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CI_HUMAN
Q5VYK1_HUMAN PRELIMINARY;
Q5VYK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSVIPEYFSGPGTPLTGNAATEE-VRGNPRDL-RVSDPTTST 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVTAAFRSGRESALSAKACTPDGFRFRFRFVFRAFTFGTAS 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDEVTVVEPASSTSVVLSSLKPETLYLVNVTAEYEDGFSIPLAGEETTEEVKGAPRNLKV
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  Extracellular matrix; Repeat; Structural protein. 3063 AA; 333147 MW; EA38CAFECE8393D2 CRC64;
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Last annotation updat
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Best Local Similarity
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                                                                                                                                                                         Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.;
"Complete primary structure of two splice variants of collagen XI
and assignment of alpha i(XII) collagen (COL12A1), alpha i(IX)
collagen (COL9A1), and alpha i(XIX) collagen (COL19A1) to human
chromosome 6q12-q13.";
Genomics 41:236-242(1997).
-i- FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COL1 domain could be associated with
surface of the fibrils, and the COL2 and NC3 domains may be
localized in the perifibrillar matrix (By similarity).
-i- SUBUNIT: Trimer of identical chains each containing 190 kDa o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOCA1 HUMAN STANDARD;

099715; 099716;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last seq

10-MAY-2005 (Rel. 37, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collagen alpha 1(XII)
Name=COL12A1;
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97288521;
                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                     Event=Alternative splicing, Named isoforms=2;
Comment=The final tissue form of collagen the collagen of collagen to soform Long or isoform combination of isoform Long and isoform Sho
                                                                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                                                                             nontriple-helical sequences.
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                                                                 homotrimers of combination of
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                                      IsoId=Q99715-1;
     IsoId=Q99715-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAAR
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                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9143499; DOI=10.1006/geno.1997.4638;
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29.9%;
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Last annotation update)
chain precursor.
                                    Sequence=Displayed;
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Pred. No. 1e-19;
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ng or isoform
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form Short or an
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PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; WWFA, 4.
Alternative splicing; Cell adhesion; Collagen;
Alternative splicing; Cell athesion; Collagen;
Hydroxylation; Repeat; Signal; Structural proteir
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Potential
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EMBL; U73779; AAD40483.1; -;
HSSP; P18614; IMHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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InterPro; IPR002035; VWF A.
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GO; GO:0001501; P:skeletal
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MIM; 120320; -.
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PTM: O-glycosylation of isoform Long; glycosaminoglycan of chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).

PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Found in collagen I-containing tissues: isoform Short and isoform Long appear in amnion, chorion, shousele, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swiss-Prot entry is copyright. It is produced through reen the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European
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                                                                                                                                                                                                                                                                                   Fibronectin type-III 3
Fibronectin type-III 4
Fibronectin type-III 6
Fibronectin type-III 7
Fibronectin type-III 7
Fibronectin type-III 7
Fibronectin type-III 7
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  TQEVTVRGDTTNTVLQGLKEGTQYALSVTALYASGAGDALFGEGTT
                                          AORVEVPAGRNCTTLOGLAPGTAYLVTVTAAFRSGRESALSAKACT
                                                                                            SGPGTPLTGNAATEEVRGNPRDLRVSDPTTSTMKLSWSGAPGKVKQ--YLVTYTPVAGGE
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.imperfections...
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.Cell attachment site (Potential).
.Cell attachment site (Potential).
.Cell attachment site (Potential).
.Hydroxyproline (By similarity).
.Hydroxyproline (By s
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N-linked (GlcNAc...
N-linked (GlcNAc...
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O-linked (Xyl.
(Potential).
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Pred. No. 1.5e-19;
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W; 75FEA78FA8E48293 CRC64;
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(Potential).
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Q4SD22_TETNG
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
A Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolicc L., Poulain J., De Berardinis V.,
A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Kindblad-Tok K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
The early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen;
NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei; Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00060; FN3; 11.
SMART; SM00127; VMA; 3.
PROSITE; PSS0853; FN3; 12.
PROSITE; PSS0234; VWFA; 3.
Collagen; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2005 (TrEMBLrel. 31, Cre
13-SEP-2005 (TrEMBLrel. 31, Las
13-SEP-2005 (TrEMBLrel. 31, Las
13-SEP-2005 (TrEMBLrel. 31, Las
Chromosome 14 SCAF14645, whole
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Q4SD22;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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PRINTS; PRO0453; VWFADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00041; fn3; 11. Pfam; PF00092; VWA; 3.
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InterPro; IPR003962; FnIII_s
InterPro; IPR002035; VWF_A.
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                                                                                              RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
QEPAANLRNSDVEIFAVGVKDAVRSELEAIANAPAETHVYTVEDFDAFQRISTELTQSIC
                                                  GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKH------
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AA; 1
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                 Score 411.5; DB 2
Pred. No. 3.6e-19;
4; Mismatches 180
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RESULT 15
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15-JUL-1998 (Rel. 36, C
28-FEB-2003 (Rel. 41, I
10-MAY-2005 (Rel. 47, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2005 (Rel. 41, Last sequence update)
Collagen alpha 1(XII) chain precursor.
Mume=Coll2a1;
Mus muscritt
                                                                                                                                                "Structural variation of type XII collagen at its carboxyl-terminal NC1 domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274.22053-22059(1999)
-i- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrilar matrix (By similarity).
-i- SUBUNIT: Trimer of identical chains each containing 190 kDa of
                                                                                                                                                                                                                                                                                                                                                     AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and sho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                      -
                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
MEDLINE=99348349; PubMed=10419532; DOI=10.1074/jbc.274.31.22053;
Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R
Olsen B.R., Nishimura I;
                                                                                                                                                                                                                                                                                                                                                                   PARTIAL NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                     development."
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of the long and short splice variants collagen XII and their tissue-specific expression during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J, and Swiss Webster; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XIIB-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING (ISOFORMS XIIA-1 AND
                                                   Name=XIIA-1
                                                                                  Event=Alternative splicing; Named isoforms=4; Comment=The final tissue form of collagen X
                                                                                                                   nontriple-helical sequences (By similarity). ALTERNATIVE PRODUCTS:
                    Name=XIIA-2;
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                                IsoId=Q60847-1; Sequence=Displayed;
                                                                 homotrimers or any combination
     ime=XIIA-2; Synonyms=ER#K;
IsoId=Q60847-2; Sequence=
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     SMAK,;
SMART; SM00327; vwm;
SMART; SM00327; vwm;
PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; VWFA; 4.
Alternative splicing; Cell adhesion; Collagen;
Alternative splicing; Repeat; Signal; St
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SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
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InterPro; IPR002035; WWF_A.
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EMBL; U57095; AAB07047.1; -; mRNA.
HSSP; P18614; 1MHP.
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Fibronectin type-III
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Extracellular matrix;

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This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                     chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collager interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
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                                                                                                          long as its content is in no way modified and this statement
ENSMUSG00000032332; Mus musculus.
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                                                        mRNA.
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O-linked (Xy)
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O-linked (Xy)
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Pred. No. 1.5e-18;
4; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                      (Potential).
                                                                                                                                                                                                                                   /FTId=VSP_001151.
Missing (in isoform XIIA-2 and isoform XIIB-2).
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N-linked (GlcNAc. ..) (Potential).
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Nonhelical region (NC3).
Triple-helical region (COL2)
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EPY -> GSG (in is
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W; 9B1F999C86AB3251 CRC64;
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ID AAE3
           Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
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             WPI; 2003-111873/10.
N-PSDB; AAD50399.
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                                                                Bateman JF, Fitzgerald DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
                                                                       Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; parkinson's disease; Alzhelmer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostacic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; hatmostatic; vulnerary; fungicide; antibacterial; virucide; protozoacid
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                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 1721.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 445
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Pred. No. 2.6e-179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cr The invention relates to an isolated polynucleotide (I) comprising a concleotide sequence selected from any of 948 sequences (ABZ1119-CR ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for cidentifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP69902-ABP6949) are useful as molecular weight complement, for generating antibodies, in medical commarkers, as a food supplement, for generating antibodies, in medical commarkers, as a food supplement, for generating antibodies, in medical compositions are useful as molecular weight compositions are useful as molecular weight compositions are considered and for treating cell-compositions are considered and for treating cell-compositions are diseases (multiple sclerosis, compositions) autoimmune diseases (multiple sclerosis, compositions) genetic disorders, myeloid or lymphoid disorders, liver lung fibrosis, infections (bacterial, viral, fungal, parasitio), compositions, compos
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Matches 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
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                                                                                                             KEQLFAEASGARPGVPKVLVMVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
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Yang Y,
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TRPGEAGPGASGPESGAGPAPTQLAALPAPEEAGPERIVISHARPRSLRVSWAPALGSAA
                                                                                     GYYVLELVPSAQPGAARRQQLPGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVR
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Pred. No. 3.2e-177;
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Drmanac RT;
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                                 PEEAGPERIVISHARPRSLRVSWAPALGSAA
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Ghosh M;
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03-JUN-2002; 2002US-0385120P.
04-JUN-2002; 2002US-0386041P.
05-JUN-2002; 2002US-0386041P.
06-JUN-2002; 2002US-0386041P.
06-JUN-2002; 2002US-0386376P.
06-JUN-2002; 2002US-0386864P.
06-JUN-2002; 2002US-0386864P.
07-JUN-2002; 2002US-0386816P.
07-JUN-2002; 2002US-0386931P.
07-JUN-2002; 2002US-0386931P.
07-JUN-2002; 2002US-0386971P.
07-JUN-2002; 2002US-0387762P.
07-JUN-2002; 2002US-038764P.
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07-JUN-2002; 2002US-0387668P.
07-JUN-2002; 2002US-0387762P.
07-JUN-2002; 2002US-0387859P.
07-JUN-2002; 2002US-0387934P.
07-JUN-2002; 2002US-0387934P.
07-JUN-2002; 2002US-0389793P.
07-JUN-2002; 2002US-0389914P.
07-JUN-2002; 2002US-0389118P.
07-JUN-2002; 2002US-038914P.
07-JUN-2002; 2002US-038914P.
07-JUN-2002; 2002US-038914P.
07-JUN-2002; 2002US-038974P.
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07-JUN-2002; 2002US-038974P.
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07-JUN-2002; 2002US-038991P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obesity; diabe
dyslipidaemia
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17-JUL-2002;
06-AUG-2002;
09-AUG-2002;
12-AUG-2002;
12-AUG-2002;
12-AUG-2002;
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2002US-0403438P.
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2002US-0403517P.
2002US-0406317P.
2002US-0406317P.
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2002US-04063182P.
2002US-04063182P.
2002US-0416352P.
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Padigaru M, Rieger DK, Smithson G, Zhong H; Alsobrook JP, Catterton E, (Ettenberg S, (Gusev VY, Her: Maclachlan (JP, Alvarez E, Anderson DW, Boldog FL, Cass, R, Chapoval A, Crabtree-Bokor JR, Edinger S. J S, Gangolli EA, Gerlach VL, Gorman L, Gunt J W, Kekuda R, Li L, Liu X, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Min T, Malyankar UM, Mezick AJ, Millet I, Mis M, Pantturajan M, Pena CEA, Peyman JA, Raha K, Rothenberg ME, Sciore P, Shenoy SG, Shimk G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ Herrmann JL, T, Malyanka Boldog FL, Casman Voss EZ, Raha D, Ras Shimkets RA; , Casman SJ;
nger SR, Ellerman
Gunther E, Guo Mishra VS; x, Macdougall Rastelli L; × ß,

N-PSDB; ADH71105. 2004-081935/08

New NOVX polypeptides and nucleic acid molecules useful for preventing treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics. 9

Example ۲, SEQ ID NO 2; 1880pp; English.

The invention relates to a novel isolated polypeptide (NOVX). A CC polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and cc neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and cc antilipaemic activity, and may have a use in gene therapy, and as a cc arcive. The polypeptides are encoded by NOVX polymucleotides comprising capetification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polymucleotide and antibody are useful in diagnosing, creating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence crepresents a NOVX polypeptide of the invention.

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Best Local
                                       Disulfide-bond
                                                                                                                                                                                                                                                            gene therapy;
                                                                                                                                                                                                                                                                         Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP;
                                                                                                                                                                                                                                                                                                               Mouse Willebrand Factor A domain related-protein (WARP).
                                                                                                                                                                                                                                                                                                                                                                                              AAE32501 standard;
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                                   /note= "O-glycosylation 369..393
                                                                                                                                                                                                         Location/Qualifiers
            /note= "0-glycosylation site"
                                                                           /note= "N-glycosylation
                                                                                                                              /note= "O-glycosylation
                                                                                                                                                                               /label=_Signal_peptide
                                                                                                     note= "N-glycosylation"
                                                                                                                                                        'note= "Mouse mature WARP protein"
                                                                                                                                                                                                                                                                                                                                                                                            protein;
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Pred. No. 3.26
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Matches 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
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                                                                                            TRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNC
                                                                                                                                              GYYVLELVPSGKLATTRRQQLPGNATSWTWTDLDPDTDYEVSLLPESNVHLLRPQHVRVR
                                                                                                                                                                                                                      AASAPAEKHLHFVDVDDLPIIARELRGSITDAMQPQQLHASEVLSSGFRLSWPPLLTADS
                                                                                                                                                                                                                                                                                              KEQLFAEEAGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTIFIVSTGRGNLLELLA
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TTVQGLTPCTTYLVTVTAAFRSGRQRALSAKACTASGARTR---APQSMRPEAGPREP
                                  TTLQGLAPGTAYLVTVTAAFRSGRESALSAKACTPDGPRPRPRPRPRPRPTPGTASREP
                                                                        TLQEEAGPERIVISHARPRSLRVSWAPALGPDSALGYHVQLGPLQGGSLERVEVPAGQNS
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Pred. No. 1.4e-135;
2; Mismatches 59;
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RESULT 5
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ID AAW8
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AC AAW8
 AAW86326;
                  AAW86326
                  standard;
                 protein; 421
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                                                                                                                                                                                                                                                                                                                 The present sequence represents a kidney injury associated molecule (KIM) CC protein. KIM proteins can be administered therapeutically by expressing CC KIM encoding polynucleotides, to promote growth and/or survival of CC damaged tissue (e.g. renal tissue), since the KIM proteins are upregulated in injured or regenerating (especially renal) tissues. KIM CC fusion proteins, conjugates, antibodies and vectors can also be used CC therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/CC prophylaxis of conditions associated with disfunction/disregulation of CC KIM genes or proteins, especially renal diseases or impairments of renal function in humans (e.g. acute renal failure, acute nephritis). The CC polynucleotides can be used to produce antisense sequences which, when CC internalised into cells, can disrupt expression of a cellular KIM gene, also useful in therapy (e.g. to block the growth of tumours dependent on CC KIM for growth) or compositions. The proteins and polynucleotides are CC (indicative of increased risk, or presence of, renal injury or impaired function), or abnormal responses to tissue injury (indicative of increased risk, or presence of, renal injury impaired CC useful diagnostically e.g. to detect and quantify renal injury or impaired condicative of increased risk, or presence of, renal injury impaired tissue of to locate KIM-producing/express to tissue injury (indicative of converted tissue), or abnormal tissue in tissue arising compositions producing cells (especially specific loci, e.g. tissue from/affecting renal tissue), by contacting cells with an imageable KIM-by by contacting cells with an ima
                                                                                                                                                                                                     Query Match
Best Local S
Matches 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kidney injury-associated molecule, KIM, injured or regenerating tissues, useful
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                                                                                                                                                                                                                                                                                      Sequence
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                                                           MLPWTALGLALSIRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA 180
                                        VATMPFGPGALRASLVHVGSRPHTEFTFDQYSSGQAIQDAVRVAPQRMGDTNTGLALAYA
                                                                                                                         MLFWTVLSMALSLRLALAQSGIERGPTASAPQGDLLFLLDSSASVSHYEFSRVREFVGQL
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77.8%;
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                                                                                                                                                                                                     Score 1643.5; DB 2
Pred. No. 1.1e-134;
1; Mismatches 59;
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antithanaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                       Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                          Claim 11; Page 3880-3881; 5507pp; English.
                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
N-PSDB; AAC76790.
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORFX open reading frames 1 to 3161.

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Best Local
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                                                    08-JUL-1999; 99JP-00194179
11-JAN-2000; 2000JP-00118775
02-MAY-2000; 2000JP-00183766
                                                                                                                           07-JUL-2000; 2000EP-00114090
                                                                                                                                                                                                   EP1067182-A2
                                                                                                                                                                                                                                                                        Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB88340 standard;
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                    (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                             or secretory protein clone PSEC0053.
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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Pred. No. 2.7e-110;
0; Mismatches 16;
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RESULT 8 ADY63045 ID ADY6

ADY63045

standard; protein;

GYYVLGLVPSAQPGGCKTPAAARER

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02-JUN-2005

(first entry)

Gene therapy

Human clone PSEC0053 protein,

SEQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc which encode human secretory or membrane proteins represented by AAB88317
cc AAB88419. Included in the invention are primers AAP93917 - AAP84295 and Cc AAF62232 - AAF62235 which are used to isolate the CDNA sequences of the Cl AAF62232 - AAF62235 which are used to isolate the CDNA sequences of the Cl AAF62232 - AAF62235 which are used to isolate the CDNA sequences of the Cl AAF62232 - AAF62235 which are used to relate methods for the production of the Cl AAF62232 - AAF62235 which are used to the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene ct therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated Cc with inappropriate secretory protein/membrane protein expression. The cu nucleic acids and complementary sequences may also be used as DNA probes ci and diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. Cc polypeptides may be used as antigens in the production of secretory proteins/membrane polypeptides and their role in metabolism. The cc polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and activity. The antibodies and activity. The antibodies and antagonists for detecting the presence of the polypeptides in samples (e.g. by enzyme cc linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim
Matches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to nucleic acid sequences AAF93744 -
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                                                                                                                                                      KEQLFAEASGARPGVPKVLVWVTDCGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA 180
                                                                                                                                                                                                                                 VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA 120
                                                                                                                                                                                                                                                                                                                  MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
GYYVLELVPSAQPG----AARRQQ 260
                                                                    AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
                                                                                                                           285 AA;
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Pred. No. 6.7e
2; Mismatches
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.7e-104;
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RESULT 9
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Best Local Sim:
Matches 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1999; 99JP-00194179.
11-JAN-2000; 2000JP-001183766.
02-MAY-2000; 2000JP-001183766.
07-JUL-2000; 2000EP-00114090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polynucleotide encoding human secretary proteins or membrane proteins, useful for examination and diagnosis of abnormality of
                22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 48; 1240pp; English
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                                                                                                                                                                      GYYVLELVPSAQPG----AARRQQ 260
                                                                                                                                                                                                                     AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
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                                                                                                                                            GYYVLGLVPSAQPGGCKTPAAARER 265
                                                                                                                                                                                                      AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
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Pred. No. 6.7e-104;
2; Mismatches 2;
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foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIZheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gastrointestinal disorder; minection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene 3 encoded secreted protein HNTEO78,
                                                                                                                                                                                                                                                                                                                                                                            secreted protein; proliferative disorder; cancer; tumour; abnormality; developmental abnormality; haematopoietic di
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WO200118022-A1

15-MAR-2001.

31-AUG-2000; 2000WO-US024008.

03-SEP-1999; 03-SEP-1999; 99US-0152317P 99US-0152315P

(HUMA-) HUMAN GENOME SCI INC.

Ni J, Soppet Moore Baker KP, Birse CE, Fiscella M, t DR, Young PE, Ebner R, Duan DR, PA, Shi Y, Wei Y, Florence KA; Komatsoulis GA, Ros Olsen HS, Lafleur Rosen eur DW; CA;

2001-203081/20.

preventing, treating or ameliorat Parkinson's diseases and cancers. Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Alzheimer's and

Claim 11; Page 532-533; 607pp; English.

gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human seccreted protein of the invention treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardivascular disorders, angiogenic disorders, kidney disorders. AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87411 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing,

Sequence 215

Query Match Best Local Similarity 99 97 .5%; Score Pred. 1084; No. 3 ö. DB 4; .4e-86; Length

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                      The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HAA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alpheimer's, payrings).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder;
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     haematopoietic disorders, neur
Parkinson's, Creutzfeldt-Jacob
                                                                                                                                                                                                                                                                                                                              Claim 1;
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The invention relates to a novel albumin fusion protein. The inv further relates to: a composition comprising the albumin fusion and a pharmaceutical carrier; a kit comprising the composition or albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein.

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New albumin fusion proteins, useful for diagnosing, or ameliorating diseases or disorders e.g. cancer, asthma, inflammatory bowel disease or Alzheimer's di

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disorder in a patient comprising the step of administering the albumin tusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the rucleic acid molecule of the albumin fusion protein, and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The calbumin fusion protein and its compositions have the following cartivities: cytostatic, antianaemic, antiarthritic, antiasthmatic, antiarchythmic, cardiant, nootropic, antiipaemic, nephrotropic, uropathic, neuroprotective, antipaexinsonian, tranquilizer, antidiabetic, anabolic, hypertensive, and vulnerary. The albumin fusion protein nucleic acid may be used in gene therapy to treat disorders. The albumin fusion protein fusion protein is cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer). Cc lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS, autoimmune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute autoimmune disease, inflammatory bowel disease, psoriasis or Lyme colonia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertolilerida, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertolileydig tumours), musculoskeletal diseases (e.g. giant cell tumours, hyper arrhythmia, cardiac arrest, heat valve disease, bypernatraemia or comprisination in sease (e.g. foetal alcohol syndrome, patau syndrome, Patau syndrome, Turner's syndrome, Apert Syndrome or Tay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Down's Byndrome, Patau Syndrome, Turner's Syndrome, Apert Syndrome or Tay Sachs disease), excretory diseases (e.g. urinary incontinence, urinary tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meninglis, cerebellar ataxia, attention deficit disorder, autism or obsessive compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, scleroderma, wound healing or epidermolysis bullosa). This sequence represents a therapeutic protein X relating to the albumin fusion protein of the invention. The sequence listing data for this specification was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents a therapeutic protein X relations of the invention. The sequence listing dowloaded from the USPTO website.
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                                                                                                                                    MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                   MLPWTAXGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                          50.3%;
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                                                                                                                                                                                                                                                  Score 1084; DB 8; Pred. No. 3.4e-86; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                           Length 215;
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В Ś 밁 Ś 뮍 S Query Match Best Local S Matches 214 181 121 121 61 AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRP 215 VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA

180 180 120

RESULT 12 AAB87418 XXXI AAB87418 standard; protein; 242

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Human gene 3 encoded secreted protein fragment, SEQ ID NO:159

foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification. secreted protein; proliferative disorder; cancer; tumour;

WO200118022-A1

31-AUG-2000; 2000WO-US024008

99US-0152315P. 99US-0152317P.

(HUMA-) HUMAN GENOME SCI INC

Ni J, Baker KP, Birse CE, Fiscella M, Soppet DR, Young PE, Ebner R, Duan DR, Moore PA, Shi Y, Wei Y, Florence KA; Komatsoulis Olsen HS, GA, Ros Lafleur Rosen eur DW; Š

WPI; 2001-203081/20.

preventing, treating or ameliorating Parkinson's diseases and cancers. Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and

Disclosure; Page 18; 607pp; English.

Parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin classoners (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, angiogenic disorders, kidney disorders, controlled disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and can diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the discolosure of the invention amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode AAB87414-AAB87454 represent human secreted protein fragments. The genes AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflaallergies, neurological disorders (e.g., Alzheimer's disease, inflammation,

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RESULT 13
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Matches 21
                      AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB8741-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                      Disclosure; Page 18; 607pp; English.
                                                                                                                                                                                                                                                                            preventing, treating Parkinson's diseases
                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human secreted proteins, used
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03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB87424 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted protein; proliferative disorder; cancer; tumour; abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Young Shi Y,
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99US-0152317P.
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Wei Y, F
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ner R, Duan DR,
Florence KA;
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                                                                                                                                                                                                                                                                                                      disorder, e.g. Alzheimer's
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Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215
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eur DW;
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Best Local Similarity
Matches 213; Conserv
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                                                                                                                                                                                                                                           inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia;
Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy;
sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
                                                                                                              Homo
                                                                                                                                                                                                                    arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; extracellular matrix and cell adhesion molecule; XMAD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AASAPAEKHLHFVDVDDLHIIVQELRGSILDAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
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                                                                                                                                                                                                                    anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1077; DB 4;
Pred. No. 1.5e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell adhesion molecule-18 (XMAD-18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                        antithyroid; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Location/Qualifiers
1. .171

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The present sequence is a human extracellular matrix and cell adhesion consolecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist cor antagonist are used for treating a disease or condition associated cor antagonist are used for treating a disease or condition associated cor increased expression of functional XMAD. The polynucleotides encoding XMAD are useful in somatic or germline gene polynucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally control of the correct and also for diagnosis of disorders associated with expression of XMAD. They are also used for generating hybridisation probes useful in mapping the naturally occurring genomic associated with expression of XMAD. They are also used for generating corresponding to model human diseases. Oligonucleotide or longer fragments derived from the polynucleotide sequences may be used as cused for the diagnosis of disorders associated with the expression of CXMAD, or in assays to monitor patients being treated with XMAD may be called for the diagnosis of disorders associated with XMAD. Diseases adiagnosed, prevented or treated include genetic disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, allergies, anaemia, asthma, correctial, fungal, parasitic, protozoal and helminthic infections and cancer including breast, bladder, bone marrow, brain and uterus calenoses is adenocarcinoma. Impropries melanoma and myeloma and cancer including breast, bladder, bone marrow, brain and uterus calenoses.
                                                                                                                        Query Match
Best Local S
Matches 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevtreatment of genetic, autoimmune and cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1999;
16-DEC-1999;
                                                                                                                                                                                                                                                            Sequence 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2000; 2000WO-US032990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200142285-A2
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                                                                                                                                                                                                                                                                                                                          cancer, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC
                                                                                                                                                           Local Similarity
                                  36 MFILDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 111; 135pp; English.
MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAM,
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99US-0172354P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Collagen glycoprotein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Collagen glycoprotein precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lal P,
                                                                                                                                                                                                                                                                                                                          adenocarcinoma, lymphoma, melanoma and myeloma
                                                                                                              42.6%; 5--
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Von Willebrand factor domain score"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ָשׁ
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                                                                                                                  Au-Young J;
                                                                                                                                                                                       Length 185
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60
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Query Match
Best Local Similarity
Matches 180; Conser

Conservative

0,

Mismatches

0

Gaps

42.4%; Score 913; DB 6; 100.0%; Pred. No. 2.3e-71;

DB 6; Length 180;

Sequence 180

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RESULT 15
AAB32500
ID AAB32500
ID AAB322
XX AAB32
XX AAB32
XX Wille
KW Wille
KW Wille
KW Extra
KW Gene
XX Homo
XX Key
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                                                                                        The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA) domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by GGG" Misc-difference 179. .180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 72-73; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2001; 2001AU-00004701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2002; 2002WO-AU000542
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                                                                   is preferably arthritis. The invention is also used present sequence is human VA domain
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DB; AAD50397.
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1. .2
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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO?*

2: /cgn2_6/ptodata/1/pubpaa/USO8_P

3: /cgn2_6/ptodata/1/pubpaa/USO9_P

4: /cgn2_6/ptodata/1/pubpaa/US10B_S

5: /cgn2_6/ptodata/1/pubpaa/US10B_S

6: /cgn2_6/ptodata/1/pubpaa/US11E_F
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US016_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US118_PUBCOMB.pep:*
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US-09-789-561-165
US-09-789-561-165
US-10-883-936-165
US-10-149-819-18
US-10-699-035A-31
US-10-699-035A-31
US-10-699-035A-31
US-10-699-035A-31
US-10-177-293-61
US-10-177-293-61
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Sequence
6, Appli

20, Appl

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85, Appl

159, App

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165, Appl

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31, Appl

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918, Ap
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GENERAL INFORMATION:
APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILLING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILLING DATE: 2002-05-02
PRIOR FILLING DATE: 2002-05-02
PRIOR FILLING DATE: 2001-05-02
NUMBER OF SEQ ID NUMBER: AU PR4701/01
PRIOR FILLING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTMARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 6
LENGTH: 418
TYPE: PRT
COGANISM: Homo sapiens
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	ALIGNMENTS				
Sequence 34, Appl	3 US-09-909-320-34	915	11.8	253.5	45
Sequence 156, App	4 US-10-428-275-156	914	11.8	253.5	44
Sequence 1292, Ap	3 US-09-833-245-1292	794	11.8	253.5	43
Sequence 176, App	4 US-10-428-275-176	782	11.8	253.5	42
Sequence 8, Appli	4 US-10-074-566-8	776	11.8	253.5	41
	4 US-10-000-512-8	776	11.8	253.5	40
2769	5 US-10-723-860-2769	580	12.0	259	39
Sequence 27, Appl	4 US-10-699-035A-27	184	12.2	263.5	38
57,		755	12.3	264	37
Sequence 22, Appl	4 US-10-699-035A-22	182	12.3	265.5	36
•	4 US-10-408-765A-17	843	12.5	268.5	35
	3 US-09-976-782-38	176	12.7	272.5	34
Sequence 10, Appl	4 US-10-115-479-10	1780	15.1	326	33
Sequence 919, App	5 US-10-631-467-919	1899	16.7	360	32
36,		87	16.9	365	31
40, A		87	17.0	366	30
•	5 US-10-741-600-1629	2944	17.8	382.5	29
Sequence 1785, Ap	5 US-10-723-860-1785	2944	17.8	382.5	28

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Query Match
Best Local 9
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Similarity 100.0%; Pred. No. 2e-
18; Conservative 0; Mismatches
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             TRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNC
                                                                       GYYVLELVPSAQPGAARRQQLPGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVR
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APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
                                                                                                              Sequence 4, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 2e-174;
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MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL

Matches

324;

Conservative

32;

Score 1653.5; Pred. No. 7.4e. 12; Mismatches

7.4e-132;

Indels

u

Gaps

60

DB 4;

Length

Query Match Best Local Similarity

76.8**%**; 77.5**%**;

US-10-699-035A-21

ORGANISM: Mus TYPE: PRT LENGTH: 415

musculus

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APPLICANT: Fitzgerald, David;
TITLE OF INVENTION: A Molecular Marker;
FILE REFERENCE: A36056 PCT USA A 071838.0142;
CURRENT APPLICATION NUMBER: US/10/699,035A;
CURRENT FILING DATE: 2003-10-31;
PRIOR APPLICATION NUMBER: PC/AU02/00542;
PRIOR FILING DATE: 2002-05-02;
PRIOR APPLICATION NUMBER: AU PR4701/01;
PRIOR APPLICATION NUMBER: AU PR4701/01;
PRIOR FILING DATE: 2001-05-02;
NUMBER OF SEQ ID NOS: 40;
SOPTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 21;
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                                                                                                                                                                                                                                              Sequence 21, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 4
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TYPE: PRT
ORGANISM: Mus musculus
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77.5%;
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US-09-789-561-85
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Best Local Similarity
Matches 214; Conserv
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                                                                                                                                                                                                                                                                                                                    LOCATION: (7)
OTHER INFORMATION: Xaa equals any of the naturally occurring
-09-789-561-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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NUMBER OF SEQ ID NOS:
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE LOCATION: (7)
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5. US20020064818A1
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   AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRP 215
                                                                                                          VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
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Pred. No. 8.4e-84;
0; Mismatches 1
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FILE REFERENCE: PF546PCT

CURRENT APPLICATION NUMBER: US/09/833,245

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-12-21

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER: OF SEQ ID NOS: 2267

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 2096
            APPLICANT: Ni et al.

APPLICANT: Ni et al.

TITILE OF INVENTION: 52 Human secreted proteins
FILLE REFERENCE: PZ043P1

CURRENT APPLICATION NUMBER: US/10/883,936

CURRENT FILING DATE: 2004-07-06

FRIOR APPLICATION NUMBER: US/09/789,561

PRIOR FILING DATE: 2001-02-22

PRIOR APPLICATION NUMBER: PCT/US00/24008

PRIOR FILING DATE: 2000-08-31

PRIOR PRIOR PHILING DATE: 1909-09-03

PRIOR FILING DATE: 1999-09-03

PRIOR PPLICATION NUMBER: 60/152,315

PRIOR PHILING DATE: 1999-09-03

PRIOR PPLICATION NUMBER: 60/152,315

PRIOR PHILING DATE: 1999-09-03

PRIOR PPLICATION NUMBER: 60/152,315

PRIOR PRILING DATE: 1999-09-03

PRIOR PRILING DATE: 1999-09-03

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US-09-833-245-2096
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                                                                                                                                                                                                                                                                                                                                                               Sequence 85, Application US/10883936
Publication No. US20050019866A1
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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NAME/KEY: SITE
LOCATION: (7)
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TYPE: PRT
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Local Similarity 99.5%;
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Pred. No. 8.4e-84
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa e
US-10-883-936-85
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CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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US-09-789-561-159
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APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 159
LENGTH: 242
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Patent No. US20020064818A1
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Best Local Similarity
                                                                      Matches
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                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids -09-789-561-159
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NAME/KEY: SITE
NAME/KEY: (2)
                                                                                                                                                                         LOCATION: (2)
OTHER INFORMATION: Xaa e
NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION: Xaa e
NAME/KEY: SITE
LOCATION: (34)
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MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFILDSSASVSHYEFSRVREFVGQL
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Pred. No. 8.4e-84;
                                                                                   Score 1084; DB 3; Pred. No. 9.9e-84;
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US-10-883-936-159
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CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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Best Local Similarity 99.5%;
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TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE LOCATION: (34) OTHER INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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OTHER INFORMATION:
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AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRP 215
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Pred. No. 9.9e-84;
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                                                                                  ; ORGANISM: Homo US-10-883-936-165
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                       FILE REFERENCE: PZ043P1

CURRENT APPLICATION NUMBER: US/10/883,936

CURRENT FILING DATE: 2004-07-06

PRIOR APPLICATION NUMBER: US/09/789,561

PRIOR FILING DATE: 2001-02-22

PRIOR APPLICATION NUMBER: PCT/US00/24008

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/152,317

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR APPLICATION NUMBER: 60/152,315
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SEQ ID NO 165
LENGTH: 226
TYPE: PRT
                                                                                                                                      PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 165
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 165, Application US/10883936 Publication No. US20050019866A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 213; Conserv
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Best Local :
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Patent No. US20020064818A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 52 Human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ni et al.
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50.0%; Score 1077; DB 5; 100.0%; Pred. No. 3.6e-83; tive 0; Mismatches 0;
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Pred. No. 3.6e-83;
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                                        Length 226;
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; OTHER INFORMATION: Incyte
US-10-149-819-18
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US-10-149-819-18
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-16; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL PROGram
SEQ ID NO 18
LENGTH: 185
TENTET
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT: BURFORD, Neil
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND
FILE REFERENCE: PF-0760 PCT
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ORGANISM: Homo sapiens
FEATURE:
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181
                              216 Q 216
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                                                                               156 QELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRP
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                                                                                                                                                96 AAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPM
                                                                                                                                                                                                              36 MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
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                                                                                                                             61 AAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPM
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Q 181
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PATTERSON, Chandra
BAUGHN, Mariah R.
LU, Dyung Aina M.
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TANG, Y. Tom
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100.0%; Pr
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Pred. No. 9.1e-70;
0; Mismatches 0;
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RESULT 13

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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699.035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PC7/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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US-10-699-035A-31
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PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                   Matches 151;
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APPLICANT: Fitzgerald, David
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VA domain from WARP
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ORGANISM: Homo sapiens
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SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 151
                                                                       | CONTINUE OF THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-699-035A-8
                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bateman, John
APPLICANT: Fitzgerald,
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                                                                                                                                                                                                 Matches
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              ORGANISM: Mus
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TYPE: PRT
181
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                                                                                  SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 151
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                                                                                                                                                                                               Conservative
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83.3%; Pred. No. 5e-57;
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Search completed: February 13, 2006, 13:12:40 Job time : 86.2776 secs

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Result
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Maximum Match 100%
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-949-016-10340
US-09-949-016-11519
US-09-949-016-11520
US-09-949-016-11520
US-09-907-794A-34
US-09-907-794A-34
US-09-906-700-34
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Sequence 6277, Ap
Sequence 57, Appl
Sequence 10341, A
Sequence 11519, A
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Sequence 1, Appl
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RESULT 2 US-09-919-497-57 US-09-919-497-57 ; Sequence 57, Application US/09919497 ; Patent NO. 6773883 ; GENERAL INFORMATION: APPLICATT: Mutter, George L. ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER ; FILE REFERENCE: B0801/7225 ; CURRENT APPLICATION NUMBER: US/09/919,497 ; CURRENT FILING DATE: 2001-07-31	Query Match 17.8; Score 384; DB 2; Length 77; Best Local Similarity 98.7%; Pred. No. 1.7e-26; Matches 76; Conservative 0; Mismatches 1; Indels 0; Gaps Qy 108 MGDTHTGLALVYAKEQLFAEASGARPGVFKVLVWVTDGGSSDFVGFPMQELKDLGVTVFI Db 1 MGDTHTGLALVYAKEQLFAEASGARPGVFKVLVWVTDGGSSDFVGFPMQELKDLGVTVFI Qy 168 VSTGRGNFLELSAAASA 184 Db 61 VSTGRXNFLELSAAASA 77	FILE REFERENCE: 59. US2.REG CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Patent.pm SEQ ID NO 6277 LENGTH: 77 TYPE: PRT ORGANIGM: Homo Bapiens FEATURE: NAME/KEY: UNSURE LOCATION: 66 OTHER INFORMATION: Xaa=Cys or Gly US-09-513-999C-6277	ESULT 1 S-09-513-999C-627 Sequence 6277, A Patent No. 67839 GENERAL INFORMAT APPLICANT: Duna APPLICANT: Duca APPLICANT: Gio TITLE OF INVENT Patent No. 67839	28 233.5 10.8 496 1 US-08-463-218-1 29 233.5 10.8 496 2 US-09-949-016-11306 Sequence 1130 30 233.5 10.8 496 4 PCT-US94-00253-1 31 233.5 10.8 405 2 US-09-312-283C-374 Sequence 374, 31 223.5 10.6 405 2 US-09-312-283C-374 Sequence 376, 32 228.5 10.4 1036 2 US-09-914-259-35 Sequence 2812 34 221 10.3 486 2 US-09-914-259-35 35 221 10.3 486 2 US-09-976-594-278 Sequence 278, 36 221 10.3 486 2 US-09-976-974-278 Sequence 278, 37 221 10.3 486 2 US-09-976-978 Sequence 278, 38 21.1 0.3 507 2 US-09-949-016-9978 Sequence 9878 39 202 9.4 1180 2 US-09-949-016-9878 Sequence 2, A 40 198.5 9.2 171 2 US-09-996-611D-1 Sequence 2, A 41 194 9.0 214 2 US-10-061-588-9 42 194 9.0 214 2 US-10-061-588-9 43 194 9.0 550 2 US-09-907-794A-227 Sequence 2, A 44 194 9.0 550 2 US-09-905-125A-227 Sequence 227, 45 194 9.0 550 2 US-09-902-775A-227 Sequence 227, 45 194 9.0 550 2 US-09-902-775A-227 Sequence 227,
NCER	; Gaps 0; DLGVIVFI 167 DLGVIVFI 60		roteins.	2225

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; PRIOR APPLICATION NUMBER: US 60/221,735; PRIOR FILING DATE: 2000-07-31; NUMBER OF SEQ ID NOS: 100; SOFTWARE: PATENTIN VERSION 3.0; SEQ ID NO 57; LENGTH: 755; LENGTH: 755; TYPE: PRT; ORGANISM: Homo sapiens
US-09-919-497-57
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US-09-949-016-10340
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 10340
LENGTH: 584
TYPE: PRT
ORGANISM: Human
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Best Local &
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
468
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ISVWAARAKEEGIVMYAVGVGKAVEAELREIASEPAELHVSYAPDFGTMTHLLENLRGSI
                                    VGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 209
                                                                                                                    GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP---GVPKVLVWVTDGGSSDP
                                                                                                                                                             DLVLLVDGSKSVRPQNFELVKRFVNQIVDFLDVSPEGTRVGLVQFSSRVRTEFPLGRYGT
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-11519
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US-09-949-016-10341
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US-09-949-016-10341
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 11519
LENGTH: 963
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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SOFTWARE: FRATSEQ for Windows Version
SEQ ID NO 10341
LENGTH: 584
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                                                                                            Local Similarity
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Local Similarity 37.2%;
Les 67; Conservative 25
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5 TALGLALSLRL-----
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                                                                                              11.8%;
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                                                        Pred. No. 1...
3: Mismatches
                                                                                            Score 255;
Pred. No. 1.
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1es 89;
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OF DETECTION AND USES THEREOF
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OF DETECTION AND USES THEREOF
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11520
LENGTH: 963
  Sequence 1, Application US/08897443 Patent No. 5981263
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                         272 VFQK 275
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                                                                                                                                                                                                                                                                                                                             88 FGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP---GVPKVLVWVTD 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 --- PRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
                                                                                                                                                                                                                                                                                                                                                                                                            31 --- PRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 TALPLILALKMEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TALGLALSLRL-------ALARSGAERGPPASA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                     GGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHI 200
                                                                                                                                                                                                                                                                                                                                                                      CENKRADIVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFS
                                                                                                                                                                                                        GRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP----GVPKVLVWVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TALPLLLALKMEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 255; DB 2; 27.9%; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89; Indels 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
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                                                                                                                       RESULT 8
US-09-907-794A-34
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                                                           Sequence 34, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
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US-08-897-443-1
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APPLICANT: Hillman
APPLICANT: Lal, Pr
APPLICANT: Corley,
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSNOT02
CLONE: 681719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA;
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Kaser, Mathew
TITLE OF INVENTION: HUMAN MATRILIN-3
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                 191 --HFVDVDDLHIIVQE 204
219 VANÉSQIETÉTSVEÇK 234
                                                                                                     134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL--
                                                                                                                                                                                                                                  99 LOYGSTVKNEFSLKTFKRKSEVERAVKRMRHLSTGTMTGLATOYALNTAFSEAEGARPLR
                                                                                                                                                                          76 VHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP-- 133
                                                                                                                                                                                                                 45 ALLESSCEN-----KRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGL
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                      ENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFL
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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31.6%; Pred. No. 9.9e-14;
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36,749
PF
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                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                   Length 638;
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David

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Query Match
Best Local Similarity
"hrches 62; Conserva
                                                                                                ; ORGANISM: Homo sapiens US-09-907-794A-34
                                                                                                                                                       SEQ ID NO 34
LENGTH: 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                NUMBER OF SEQ ID
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PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TILE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15
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FILING DATE: 1999-09-13
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FILING DATE: 1999-09-08
                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US99/30999
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/21547
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/28564
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Eaton, Dan
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                    Conservative
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art, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicholas F.
                                                                                                                                                                                                                                                          1999-12-20
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f, Ellen
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                                    11.8%;
                    36;
                  Score 253.5; DB 2;
Pred. No. 1.6e-13;
6; Mismatches 85;
                    Indels
                                                         Length
                                                         915;
                  13;
                  Gaps
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ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL

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APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: U$/09/905,125A

CURRENT EILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR APPLICATION NUMBER: U$ 60/143,048

PRIOR FILLING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: U$ 60/145,698

PRIOR APPLICATION NUMBER: U$ 60/146,222

PRIOR APPLICATION NUMBER: U$ 60/146,222

PRIOR FILLING DATE: 1999-07-28

PRIOR FILLING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: U$ 60/146,222

PRIOR APPLICATION NUMBER: BCT/US99/20594
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                                                      PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
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Patent No. 6664376
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APPLICANT:
APPLICANT:
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APPLICANT:
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FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart,
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
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Filvaroff, Ellen
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Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. Mickey
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RESULT 10
US-09-902-775A-34
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SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local
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APPLICANT:
        APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP--
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                                                                                                                                                                              Godowski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi, Avi
Botstein, David
                                                                                      Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
                                                                                                                        Paoni,
                                                                                                                                                    Kljavin, Ivar J.
Mather, Jennie P.
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Eaton, Dan L.
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                                                                                                                   James
11, Nicholas F.
10466-14
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                                                                                                                                                                                                                                                                                                                 Sherman
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Pred. No. 1.6e-13;
6; Mismatches 85
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US-09-906-700-34

Sequence 34, Application US/09906700 Patent No. 6723535
GENERAL INFORMATION:

APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi APPLICANT: Botstein, David

APPLICANT:

Desnoyers,

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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR; FILING DATE: 2000-02-22
PRIOR REPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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SEQ ID NO 34
LENGTH: 915
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Best Local S
Matches 62
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/30911
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FILING DATE: 1999-12-02
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219 VANFSQIETLTSVFQK 234
                                                  191 --HFVDVDDLHIIVQE 204
                                                                                                 159 ENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFL
                                                                                                                                              134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL--
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                                                                                                                                                                                                                                                                                                                 16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
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                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 253.5; DB 2; ilarity 31.6%; Pred. No. 1.6e-13; Conservative 36; Mismatches 85;
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APPLICANT:

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                                                                                                                               ; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-34
                                                            Matches
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Best Local Similarity
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR FILING DATE: 2000-02-2
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                        ch 11.8%; Score 253.5; DB 2
l Similarity 31.6%; Pred. No. 1.6e-13;
62; Conservative 36; Mismatches 85
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Mather, Jennie P.
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Grimaldi, Christopher
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Gerritsen, Mary E.
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Ferrara, Napoleone
Filvaroff, Ellen
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: GNE.1618P2C12 CURRENT APPLICATION UNMER: US/09/903,603A CURRENT FILING DATE: 2001-07-11 PRIOR APPLICATION NUMBER: PCT/US00/04414 PRIOR FILING DATE: 2000-02-22 PRIOR APPLICATION NUMBER: US 60/143,048 PRIOR FILING DATE: 1999-07-07 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR FILING DATE: 1999-07-26 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR FILING DATE: 1999-07-28 PRIOR APPLICATION NUMBER: US 60/146,222 PRIOR APPLICATION NUMBER: US 60/146,222 PRIOR APPLICATION NUMBER: US 70/146,222 PRIOR APPLICATION NUMBER: US 70/146,222 PRIOR APPLICATION NUMBER: US 70/146,222 PRIOR APPLICATION NUMBER: PCT/US99/20594 PRIOR APPLICATION NUMBER: PCT/US99/20944 PRIOR APPLICATION NUMBER: PCT/US99/20944 PRIOR APPLICATION NUMBER: PCT/US99/20944 PRIOR APPLICATION NUMBER: PCT/US99/20944 PRIOR APPLICATION NUMBER: PCT/US99/21090
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
                                                                                                                  FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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Williams, P. Mickey
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
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Filvaroff, Ellen
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Eaton, Dan L.
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Botstein, David
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PRIOR FILLING DATE: 1999-12-16
PRIOR FILLING DATE: 1999-12-16
PRIOR FELLING DATE: 1999-12-10
PRIOR FILLING DATE: 1999-12-20
PRIOR FILLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILLING DATE: 1999-12-20
PRIOR FILLING DATE: 2000-01-05
PRIOR FILLING DATE: 2000-01-05
PRIOR FILLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                  APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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APPLICATION NUMBER: US/09/904,920A
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
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                                                                                                                 Roy, Margaret Ann
Stewart, Timothy A.
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Grimaldi, Christopher
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Gerritsen, Mary E.
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Filvaroff, Ellen
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36; Mismatches 85
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                                                                                               GENERAL INFORMATION:
                                                                                                                 Sequence 34, Application US/09909064 Patent No. 6818449
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SEQ ID NO 34
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                                     APPLICANT: Genentech,
APPLICANT: Ashkenazi
APPLICANT: Botstein,
  APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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TYPE: PRT
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FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/28214
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                                                                                                                                                                                                                                     219 VANÉSQIETÉTSVFQK 234
                                                                                                                                                                                                                                                                          191 --HFVDVDDLHIIVQE 204
                                                                                                                                                                                                                                                                                                                                                    134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL-- 190
                                                                                                                                                                                                                                                                                                                                                                                              99 LQYGSTVKNEFSLKTFKRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLR
                                                                                                                                                                                                                                                                                                                                                                                                                             76 VHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLESSCEN-----KRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGL
                                                                                                                                                                                                                                                                                                               ENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFL
Desnoyers,
Eaton, Dan
                                   Ashkenazi, Avi
Botstein, David
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                                                         Inc.
Avi
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Pred. No. 1.6e-13;
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APPLICANT:

Filvaroff,

Napoleone f, Ellen

Fong,

Wei-Qiang

PPLICANT:

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US-09-909-064-34
                                                                                       Query Match
Best Local 9
                                                                                                                                                                                             SEQ ID NO 34
LENGTH: 915
                                                                      Matches
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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                                                                                                                                                          LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/145,698 FILING DATE: 1999-07-26
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APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US99/30999
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45
                                 16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                                    | Similarity | 62; Conserv
ALLESSCEN-----KRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGL
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Mather, Jennie
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Grimaldi, Christopher
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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                                                                        Conservative
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                                                                                       11.8%;
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                                                                    36;
                                                                    Score 253.5;
Pred. No. 1.6e
36; Mismatches
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                                                                    . 1.6e-13;
tches 85;
                                                                                                        DB 2;
                                                                                                        Length 915;
                                                                        Indels
                                                                        13;
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RESULT 15
US-09-905-381A-34
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SecurITITLE OF INVENTION: Acids Encoding the saw TITLE OF INVENTION: Acids Encoding the saw CITLE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT APPLICATION NUMBER: 2001-07-13
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-11-29
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                                                                                                                                   FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
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o. 6818746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T: WOOD, William, I.
INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Ashkenazi, Avi
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Gerritsen, Mary E
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Filvaroff, Ellen
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Botstein, David
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Mather, Jennie P.
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Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ni, Nicholas F., Margaret Ann wart, Timothy A.
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30091
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 1990-12-20
PRIOR FILING DATE: 1990-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
LENGTH: 915
TYPE: PAT
ORGANISM: Homo sapiens
US-09-905-381A-34
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Search completed: February 13, 2006, 07:50:52 Job time : 65.3077 secs
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                                                                                                       191 --HFVDVDDLHIIVQE 204
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Maximum DB
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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10699035/runat_13022006_062447_25513/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US10699035/runat_13022006_062447_25513/app_query.fasta_1
-DB=Issued_patents_AA_OFMT=fastan_SUFFIX=rai_MINMATCH=0.1 -LOOFCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=set -HAPSIZE=500 -MINIEN=0 -MAXIEN=2000000000
-HOST=abss02p -USER=US10699035 @CGN 1 101 @runat 13022006 062447 25513
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NORM=set -NORM=
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ALIGNMENTS

US-09-513-999C-6277

Sequence 6277, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.

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APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59. US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 6277

LENGTH: 77

TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
PRATURE:
NAME/KEY: UNSURE
LOCATION: 66

OTHER INFORMATION: Xaa=Cys or Gly

US-09-513-999C-6277

Alignment Scores:
Pred. No.:
161e-18
Best Local Similarity: 98.7%
Best Local Similarity: 98.7%
Best Local Similarity: 98.7%
Best Local Similarity: 98.7%
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LENGTH: 860
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Qy 416 418	Qy 379 GAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGC 415	Qy 319 CGCATGGGTGACACCCACACTGGCCTGGCCTGGTCTATGCCAAGGAACAGCTGTTTGCT 378	Qy 259 CCTTCGGCCAGCACAGCTCGGGTGAGGCTGCCCAGGATGCGGTGCTTCTGCCCAG 318 :::::		Db 79 sTrpLysThrArgAsnValAlaGlyArgSerAlaThrAspAlaTrpSerSerAlaPro 98	Qy 178 CTGG198	Qy 142 TACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGCAG 177	Oy 96AGAGGACCIGATGITCCTGCTGAGCAGCCTCTCAGCCAGCCTCTCACC 141	23 OIIDSETINTINTAIGPFOPFOALAASDAIGSETGIYALATINTALAAIGVALPTOAL	75TCCACCAGCATCAGCCCCCG	Db 8 AlaTrpProGlnArgTrp-ProProArgArgAlaAlaArgAlaSerPr 23	сттесеестеесестеесее	10-699-035A-5 (1-1254) x US-09-252-991A-30843 (1-66	11.8% Indels:	: 281.50 Macches: The Conservative: 29.4% Conservative: 29.4% Conservative: 24.0% Minimate Conservative	_	; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30843	; SEQ 1D NO 30843 ; LENGTH: 663 ; TYPE: PRT		; PRIOR FILING DATE: 1998-02-18 ; PRIOR APPLICATION NUMBER: US 60/094,190	APPLICATION NUMBER: 1	FERENCE: 107196.136 APPLICATION NUMBER: US/09/252,991A	; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS	; Patent No. 6551795 ; GENERAL INFORMATION:	œΝ	devisestinantinationisticitati	
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519 roArgProAlaIleProAlaHisArgProSerAlaSerAlaThrGlyTrpP 536		:: rgArgAlaArgThrGlyIleArgArgThrAlaAlaAlaAlaCysTyrProProProAlaP rgArgCCTGCGGGTGCGCACGCGGCCAGAGGGCCAGAGCGCAFCGTCAFCTCC	:::	443 oIleAlaGlySerAlaProGlySerGlyThrAlaProArgCysHisProValArgLysAs 463	799 799	796 GACT	CLABSTOCKSGGGT ISCANGATOCK AGENGT ISCANGGGTANGGTANGGTANGGT ISCANGGGTANGGTANGGTANGGTANGGTANGGTANGGTANG	aGlyArgLeuArgArgValArgArgSerAlaArgArgAlaTrpArgProTrpProAl	748 748	363 lAlaAlaTrpAlaProAlaArgGlyGlyTyrAlaAlaAlaProArgAsnSerCysSerAl 383	343 INSTRUCTION PROCESSING TO THE TRANSPORT OF THE TRANSP	686TGGCCTGGCCACCCCTGCTGAGACTCGGGCTACTATGTG 729	323 oCysValProAsnCysValAsnTrpArgArgIleProTrpSerAlaValAlaLysTh 343	659 685	303 aCysGlyHisAspGlyAspAlaGlyArgAlaSerGlnThrProTrpArgAspThrSerPr 323	838	583 GTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTCGCGA 634	 263 aAlaCysProThrThrTrProProAlaAsnAlaProAlaSerAlaAlaAsnTrpPr 283	545	::: 243 aArgProSerAlaIleAlaSerThrAlaArgArgSerProSerThrAsnGlyArgProAl 263	535 TCAGCCGCTG 544	 	203 OAGTRIGATIYSETATATIYDYBKTGCYBATACYBATACYBATACATGTYSETAT 223	CAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGC	185 sGlyArgProProAlaCysSerProValAlaThrAlaProThrAlaThrCysSerProPr 205	419TGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCCC 462	165 gArgArgArgGluProTrpProProSerProTyrAlaSerArgAlaGlyProAlaSerCy 185

	Db 38 a	1085 AGCGTGGTGCAGTTGCGGCCCGCGGGGCACCTCCCCCCCC	OY 1145 CCCGAGCGGAAGGCGGTCACGGTCACGGTAGGCGGTGCCCGGCGCCAGGCCCTGC 1086	Oy 1205 CGTGGGCGCGGGCGGGCCGTCGGGCGTGCAGGCCTTGGCGACAGCCGCTCTCGCGG 1146	US-10-699-035A-5 (1-1254) x US-09-252-991A-26078 (1-511)	Match: 11.7% Indels: 2 Gaps:	: 3.15e-11 279.00 imilarity: 35.8% l Similarity: 30.5%	; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26078 Alignment Scores:	NGTH: 51	; PRIOR FILING DATE: 1998-07-27 ; NUMBER OF SEQ ID NOS: 33142 . SED TD NO 26078		T APPLICAT	ION: NUCLEIC ACID ION: AERUGINOSA FO	o. 6551795 INFORMATION: VT: Marc J. Rubenfield et al.	RESULT 4 US-09-252-991A-26078 ; Sequence 26078, Application US/09252991A	9	CGCCA	Qy 1192 CGCCCGCGCCCACGCCCACGCCCCGCGCCCCGAC 1226	Db 593 oProAlaAlaThrGlyArgProSerAlaProProArgProAlaArgArgArgValAr 613	CCGCTCGGGCCGCGAGAGCGCGCGCTGTCGCAAGGCCTGCACGCC	Cy 1109	555 aProAlaProAlaProHisAlaArgProArgAlaProArgArgProGlyArgSerPr	OY 1060 CCCGCGGGCCGCAACTGCACCACGCTGCAGGGCCTGGGGGCCGGGCACCG 1108		OV 1000 CTCGGCTACCACGTGCAGTTCGGGCCGCTGCGGGGGGGGG
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341 gProprohrghrgAlahlaSerTrpSerArgAspArgAspGlyLysThrAlaAlaGlySe 361 38 AAGCTCAGGGCCAGGCCGAGCGCCGTCCAGGGGAGCA 2	71 CGCTCCGCGCCCCCGCG	321 aAlaAlaArgProArgAlaProSerIleArgThrThrGlyGlyAspGlyArgHisSerAr 341				290 GCAGCCTCACCCGAGCTGTGCTGGCCGAAGGGGAACTCGGTGTATGGCCGACTGCCCACG 231	347 GCCAGGCCAGTGTGGGTGTCACCCATGCGCTGGGCAGAAGCACGCACCGCATCCTGG 291	377 GCAAACAGCIGTICCTIGGCAI		401 CCTGGCCGGGCAC378	461 GGGGGCCCACAGGGTCGCTGGAGCCGCCATCTGTCACCCACC	194ArgSerProProSerAlaThrAlaAr 202	521 TTGCCTCGGCCGGTGCTGACAATGAACACGGTGACGCCCAGGTCCTTGAGCTCCTGCATG 462	581 TCCACAAAAGTGCAGGTGCTTCTCGGCAGGGGCTGAGGCAGCGGCTGACAGCTCCAGGAAG 522	::: ::: 158 oAlaAlaAlaArgGlnProProProValArgArgGlyAlaArgGlySerAl 175	641 GGCCGCATCGCGAGAATGGAGCCCCCTCAGCTCTTGGACAATGATGTGCAGGTCATCCACG 582	701 AGGGTGGCCAGGCCAGGCGGAAGCCGCTGGACGTGATCTCCGTGGCATGGAGCTGCTGC 642	 141ProAlaValArgArgGlySerArgProAlaGlySerSerPro 154	761 GCCCCCGGCTGGGCACCAGCTCCAGCACATAGTAGCCCGAGTCTGCGGTCAGC 702	821 GGGTCGAGGCCCGAGATCCAGTCCGTGGCGTTCCCTGGCAGCTGCTGCTGGCGTTGCA 762	110 rGlyAsnArgThrGlyAlaArg	881 TGGGGCCTCAGGAGGCGCACGTTGGACTCAGGCACTAGCGCCACGTCGTAGTCCGTGTCC 822	922 -CTGGCCCGGCCT	rgArgĠĺyGlyArgAr	965 ACGCGGAGCTGCGCGGCGGCGGGGGGAGATGACGATGCGCT 923

Db 365 LeuclyClyAlaHisProArgProAlyGlnProAlaThrAlaGlyTyrArgProAlala 384 Qy 57 GAGCGGCGCGGAGCGCGGTCCACCAGCATC	RESULT 5 US-09-252-991A-17231 Sequence 17231, Application US/09252991A PATECON NO. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. APPLICANT: MUNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ITITLE OF INVENTION: AND THERAPEUTICS FILE REFERENCE: 107196.116 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 I. ENGTH: 2294 I. TYPE: PRT I. ORGANISM: Pseudomonas aeruginosa US-09-252-991A-17231 Alignment Scores: Best Local Similarity: 23.3* Oconservative: 159 Ouery Match: 11.7* DB: DB: US-10-699-035A-5 (1-1254) x US-09-252-991A-17231 (1-2294) US-10-699-035A-5 (1-1254) x US-09-252-991A-17231 (1-2294) DC: DB: DB: DB: DB: DB: DB: DB: DB: DB: DB
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 25101
LENGTH: 917
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                    GTCCGCCAAGGCCTGCACGCCCGA-----
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                                                                                                                                    CACCGCCTACCTGGTGACCGTGACCGCCCTT---CCGCTCGGGCCGCGAGAGCGCGCT 1160
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414 GCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCCATGCAGGAGCT	Qy 366 ACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGT 413	Qy 306 TGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGTCTATGCCAAGGA 365	OY 276 CTCGGGTGAGGCTGCCCAGGATGCGGTGCG 305		63GlybroGlnHishrgbroGluArgGlnbroGlyAlaGly	177 GCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCAGTCTGGTGCACGTGGG 2	Qy 132CGTCTCTCACTACGAGTTCTCCCCGGGTTCGGGGAGTTTGTGGGGCA 176	24 ArgValCysArgArgGlnArgGlnGlnGlnGlyAlaGlyValLeuGlnGlnArgGlnPro	81 AGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGACAGCTCAGCCAG	21 CGGCCTGGCCCTGAGCTTGCGGCTGGCGCTGGCGCGGA	11.4% Indels: 2 Gaps: 54) x US-09-252-991A-20375 (1-65	No.: 9.84e-11 272.00 1t Similarity: 32.9% occal Similarity: 29.0%	; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-20375 Alignment Scores:		APPLICATION N FILING DATE: FOR SECTION NO	; CURRENT FILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788 . DETOR FILING DATE: 1988-02-19	F INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FERENCE: 107196.136 APPLICATION NUMBER: US/09/252,991A	Rubenfield e NUCLEIC ACI	; Sequence 20375, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION:	991A-20375	Db 912 ArgThrPro 914	Qy 1236 CGCCAGCC 1244	Db 893 GlyAlaAlaArgAlaAlaProArgProPheProArgProGlyArgAlaThrAspGly 911
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Db 129 ArgArgAlaLeuValProAlaLeuProAlaGlyAspLeuProLeuGlnSerLeuAlaArg 148 Oy 153 CCGGGTTCGGGAGTTTGTGGGGCAGCTGGTGGTCCACTGCCCCTGGGCACCGGGGCCCT 212	Gaps:	PPLICATION NUMBER: US 60/074 ILING DATE: 1998-02-18 PPLICATION NUMBER: US 60/094 PPLICATION NUMBER: US 60/094 ILING DATE: 1998-07-27 DF SEQ ID NOS: 33142 D 28339 PRT SM: Pseudomonas aeruginosa 991A-28339 Scores: 1.28e-10 270.00 nilarity: 34.5% Similarity: 29.7% 11.38	Qy 1152 GAGCGCCTGTCCGCCAAGGCCTGCACGCCCGACGGCCCGCGCCCCACGCCC 1208
Qy 1068 CCGCAACTGCACCACGCTGCAGGGCCCGGGGCACCGCCTACCTGGAGGCCTGCACGACGGCTGCAGGCCTGCAGGGCCCGGGCACCGCCTACCTGGTGACCGTGAC 1127	Db 347 ThrTrpArgSerAlaArgArgAspArgAlaValArgPheArgGlnValAspProGlyAla 366 Qy 846AGTGCTGAGTCCAACGTGCGCCTCTGAGGCCCCAGATCCT 887 Db 367 LeuAlaGlyGlyArgLeuAlaAlaAlaAlaValArgArgGlyAlaProGlyArgArgArgPro 386 Qy 888 GCGGGTGCGCACGCGGCCAGAGGAGGCCAGAGCGCATCGTCATCTCCCACGCCG 947	Qy 609AGAGCTGAGGGGCTCCATTCTCGCGATGCGGCCGCAGCAGCAGCTCCATGCCAC	Qy 357 TGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGACGGGGTGCCCAAAGTGCT 416 Db 217

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Query Match:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 31790
LENGTH: 689

TYPE: NUMBER OF SEQ ID NOS: 33142
LENGTH: 689
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ORGANISM: Pseudomonas aeruginosa
09-252-991A-31790
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                      TGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATCAT
                                                       ProAlaArgArgCysArgProArg-----ProGlyAlaTrpArgArg--------
                                                                                          GTTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCC
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RESULT 10
US-09-252-991A-31760
; Sequence 31760, Applic
; Patent No. 6551795
; GENERAL INFORMATION:
; TITLE OF INVENTION:
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31760
LENGTH: 1706
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                     Sequence 30843, Application Patent No. 6551795
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NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30843
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Best Local Similarity:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27068

LENGTH: 638

TYPE: NEW
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                                                                     ; Sequence 57, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF
FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR PILING DATE: 2000-07-31
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                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 57 LENGTH: 755
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                                                                                                                                                                Sequence 18035, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MACC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F.
TITLE OF INVENTION: AERUGIOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT FILING DATE: 1099-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO.8: 33142
SEQ ID NO. 18035
LENGTH: 783
             Best Local Similarity:
Query Match:
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                                                                                                                                              CCCAGCCGGGGGCTGCAAGACGCCAGCAGCTGCCAGGGAACGCCACGGACTGGAT----
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                CTACGACGTGGCGCTAGTGCCTGAGTCCAACGTGCGCCTCC
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                                                                                                                                                                           Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                             APPLICATION UNDER: US 60/094,190

PRIOR FILLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

RUBDERICA ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

NUMBER: OS 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 19127

LENGTH: 590

TYPE: DET
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GENERAL INFORMATION:
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                                                                                               CGGCTGGCGGTCCCCGGGGTCGGGGCGCGCGGGCGCACGGGCGCGGGCGCGGGCCGGGCCG
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                                                                ArgLeuAlaAlaProGlyGlyGlyAlaHis-----ArgGlyAlaTrpArgAspGln
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293 gAl 421	335 gPr 402	, 0	1 ()	GTG 489	GCT 549 aLe 353	587 gPh 333	GGC 639 oAl 320	CAG 690 -Ar 300	-GC 741 oAl 282	770 uSe 262		ACG 837 222	CGC 888 0Al 202	GGC 948 184	rgg 1008 : ng1 169	sHi 151	13

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